

GenCore version 5.1.7
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CM protein - protein search, using sw model

Run on: April 13, 2006, 17:19:00 ; Search time 35.4017 Seconds
(without alignments)
282.578 Million cell updates/sec

Title: US-10-727-737-17

Perfect score: 649

Sequence: 1 EVQLVESGGGLVQPGSLRLA.....FYGTTYFDYWGQGLVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 649 | 100.0 | 121 | 2 | US-08-974-899-24 |
| 2 | 649 | 100.0 | 121 | 2 | US-09-795-798-24 |
| 3 | 632 | 97.4 | 121 | 2 | US-08-974-899-5 |
| 4 | 632 | 97.4 | 121 | 2 | US-09-795-798-5 |
| 5 | 548.5 | 84.5 | 116 | 2 | US-09-027-449-50 |
| 6 | 548.5 | 84.5 | 116 | 2 | US-08-804-444A-50 |
| 7 | 548.5 | 84.5 | 116 | 2 | US-09-026-985-50 |
| 8 | 548.5 | 84.5 | 116 | 2 | US-09-121-952A-50 |
| 9 | 548.5 | 84.5 | 116 | 2 | US-09-234-340A-50 |
| 10 | 548.5 | 84.5 | 116 | 2 | US-09-355-014-50 |
| 11 | 520.5 | 80.2 | 122 | 1 | US-07-334-373C-20 |
| 12 | 520.5 | 80.2 | 122 | 2 | US-08-437-642B-20 |
| 13 | 520.5 | 80.2 | 122 | 2 | US-08-146-206C-20 |
| 14 | 520.5 | 80.2 | 122 | 2 | US-09-705-686-20 |
| 15 | 520.5 | 80.2 | 122 | 2 | US-09-705-392A-20 |
| 16 | 520.5 | 80.2 | 122 | 2 | US-09-705-398-20 |
| 17 | 520.5 | 80.2 | 122 | 4 | PCT-US93-07832-20 |
| 18 | 512.5 | 79.0 | 253 | 2 | US-09-027-449-52 |
| 19 | 512.5 | 79.0 | 253 | 2 | US-09-027-449-55 |
| 20 | 512.5 | 79.0 | 253 | 2 | US-08-804-444A-52 |
| 21 | 512.5 | 79.0 | 253 | 2 | US-08-804-444A-55 |
| 22 | 512.5 | 79.0 | 253 | 2 | US-09-026-985-52 |
| 23 | 512.5 | 79.0 | 253 | 2 | US-09-026-985-55 |
| 24 | 512.5 | 79.0 | 253 | 2 | US-09-121-952A-52 |
| 25 | 512.5 | 79.0 | 253 | 2 | US-09-121-952A-55 |
| 26 | 512.5 | 79.0 | 253 | 2 | US-09-234-340A-52 |
| 27 | 512.5 | 79.0 | 253 | 2 | US-09-234-340A-55 |

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|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 512.5 | 79.0 | 253 | 2 | US-09-355-014-52 | Sequence 52, Appl |
| 29 | 512.5 | 79.0 | 253 | 2 | US-09-355-014-55 | Sequence 55, Appl |
| 30 | 512.5 | 79.0 | 256 | 2 | US-09-027-449-70 | Sequence 70, Appl |
| 31 | 512.5 | 79.0 | 256 | 2 | US-09-026-985-70 | Sequence 70, Appl |
| 32 | 512.5 | 79.0 | 256 | 2 | US-09-121-952A-70 | Sequence 70, Appl |
| 33 | 512.5 | 79.0 | 256 | 2 | US-09-234-340A-70 | Sequence 70, Appl |
| 34 | 512.5 | 79.0 | 256 | 2 | US-09-355-014-70 | Sequence 70, Appl |
| 35 | 512.5 | 79.0 | 298 | 2 | US-09-027-449-60 | Sequence 60, Appl |
| 36 | 512.5 | 79.0 | 298 | 2 | US-08-804-444A-60 | Sequence 60, Appl |
| 37 | 512.5 | 79.0 | 298 | 2 | US-09-026-985-60 | Sequence 60, Appl |
| 38 | 512.5 | 79.0 | 298 | 2 | US-09-121-952A-60 | Sequence 60, Appl |
| 39 | 512.5 | 79.0 | 298 | 2 | US-09-234-340A-60 | Sequence 60, Appl |
| 40 | 512.5 | 79.0 | 298 | 2 | US-09-355-014-60 | Sequence 60, Appl |
| 41 | 512.5 | 79.0 | 452 | 2 | US-09-027-449-71 | Sequence 71, Appl |
| 42 | 512.5 | 79.0 | 452 | 2 | US-09-026-985-71 | Sequence 71, Appl |
| 43 | 512.5 | 79.0 | 452 | 2 | US-09-121-952A-71 | Sequence 71, Appl |
| 44 | 512.5 | 79.0 | 452 | 2 | US-09-234-340A-71 | Sequence 71, Appl |
| 45 | 512.5 | 79.0 | 452 | 2 | US-09-355-014-71 | Sequence 71, Appl |

ALIGNMENTS

RESULT 1
US-08-974-899-24
; Sequence 24, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-24

Query Match 100.0%; Score 649; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 7,7e-57;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGSLRLAASGYSFPTGHWNVVRQAPGKGLVWGMTAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGSLRLAASGYSFPTGHWNVVRQAPGKGLVWGMTAPASSSTRY 60

QY 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 Db 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 QY 121 \$ 121
 Db 121 \$ 121

RESULT 2

US-09-795-798-24
 ; Sequence 24, Application US/09795798
 ; Patent No. 6703018
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/795,798
 ; FILING DATE: 28-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/974,899
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P1014R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 121 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear

US-09-795-798-24
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Query Match 100.0%; Score 649; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 7.7e-57;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNVRQAPGKLEWVGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNVRQAPGKLEWVGMIAPASSSTRY 60
 QY 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 Db 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 QY 121 \$ 121
 Db 121 \$ 121

RESULT 3

US-08-974-899-5
 ; Sequence 5, Application US/08974899
 ; Patent No. 6037454

; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,899
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/031971
 ; FILING DATE: 11/27/96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P1014R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 121 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-974-899-5

Query Match 97.4%; Score 632; DB 2; Length 121;
 Best Local Similarity 96.7%; Pred. No. 3.7e-55;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNVRQAPGKLEWVGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNVRQAPGKLEWVGMIHPSDSETRY 60
 QY 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 Db 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 QY 121 \$ 121
 Db 121 \$ 121

RESULT 4

US-09-795-798-5
 ; Sequence 5, Application US/09795798
 ; Patent No. 6703018
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-795-798-5

Query Match 97.4%; Score 632; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 3.7e-55;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMIAPASSSTRY 60
Eb 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMIHPSDSETRY 60
Cy 61 NQKFKDRFTISVDKSKNTLYLQNSLRADTAIVYVCARGIYFGTTFYDYGQGTIVTVS 120
Db 61 NQKFKDRFTISVDKSKNTLYLQNSLRADTAIVYVCARGIYFGTTFYDYGQGTIVTVS 120
Cy 121 S 121
Db 121 S 121

RESULT 5
US-09-027-449-50
Sequence 50, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-50

Query Match 84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Cy 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMIAPASSSTRY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMIHPSDSETRY 60
Cy 61 NQKFKDRFTISVDKSKNTLYLQNSLRADTAIVYVCARGIYFGTTFYDYGQGT 115
Db 61 ADVKGRFTISRDNKNTLYLQNSLRADTAIVYVCARGIYFGTTFYDYGQGT 116

RESULT 6
US-08-804-444A-50
Sequence 50, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-50

Query Match 84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

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QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNWVRQAPGKLEWVGMIAPASSSTRY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNWVRQAPGKLEWVGMIHPSDSETRY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQNNLSRAEDTAVYVC-ARGIYFYGTTFYDYWGQGT 115
Db 61 ADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYCAARGIYFYGTTFYDYWGQGT 116

RESULT 7
US-09-026-985-50
; Sequence 50, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-50

Query Match 84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNWVRQAPGKLEWVGMIAPASSSTRY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNWVRQAPGKLEWVGMIHPSDSETRY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQNNLSRAEDTAVYVC-ARGIYFYGTTFYDYWGQGT 115
Db 61 ADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYCAARGIYFYGTTFYDYWGQGT 116

RESULT 8
US-09-121-952A-50
; Sequence 50, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra

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; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-121-952A-50

Query Match 84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNWVRQAPGKLEWVGMIAPASSSTRY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNWVRQAPGKLEWVGMIHPSDSETRY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQNNLSRAEDTAVYVC-ARGIYFYGTTFYDYWGQGT 115
Db 61 ADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYCAARGIYFYGTTFYDYWGQGT 116

RESULT 9
US-09-234-340A-50
; Sequence 50, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

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; FILING DATE: 21-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-355-014-50
Query Match      84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1
QY      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKLEWVGMIAPASSSTRY 60
Db      1 EVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMNWVRQAPGKLEWVGMIHPDSETRY 60
QY      61 NQKFKDRFTISVDKSKNTLYLQWNSLRADTAIVYIC-ARGIFYFGTTFYDFYWGQGT 115
Db      61 ADSVKGKFTISRDNKSKNTLYLQWNSLRADTAIVYCAARGIFYFGTTFYDFYWGQGT 116

RESULT 11
US-07-934-373C-20
; Sequence 20, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA: 07/715272
; APPLICATION NUMBER:
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

```


RESULT 14
US-09-705-686-20
; Sequence 20, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09705.686
; FILING DATE: 02-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-705-686-20
Query Match 80.2%; Score 520.5; DB 2; Length 122;
Best Local Similarity 83.7%; Pred. No. 3.9e-44;
Matches 103; Conservative 4; Mismatches 13; Indels 3; Gaps 2;
QY 1 EVLVESGGGLVPGGSLRLSCLAAAGYSFTGHNNWVRQAPGKLEWVGMIAPASSSTRY 60
Db 1 EVLVESGGGLVPGGSLRLSCLAAAGYSFTGHNNWVRQAPGKLEWVGMIAPASSSTRY 60
QY 61 NQKFKDRFTISVDKSKNTLYLQNSLRAEDTAVYVCARGIYFYGTT--YFDYWGQGTTLVT 118
Db 61 NQKFKDRFTISVDKSKNTLYLQNSLRAEDTAVYVCARGIYFYGTT--YFDYWGQGTTLVT 118
QY 119 VSS 121
Db 120 VSS 122
Search completed: April 13, 2006, 17:20:46
Job time : 36.4017 secs

RESULT 15
US-09-705-392A-20
; Sequence 20, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09705.392A
FILING DATE: 02-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-705-392A-20
Query Match 80.2%; Score 520.5; DB 2; Length 122;
Best Local Similarity 83.7%; Pred. No. 3.9e-44;
Matches 103; Conservative 4; Mismatches 13; Indels 3; Gaps 2;
QY 1 EVLVESGGGLVPGGSLRLSCLAAAGYSFTGHNNWVRQAPGKLEWVGMIAPASSSTRY 60
Db 1 EVLVESGGGLVPGGSLRLSCLAAAGYSFTGHNNWVRQAPGKLEWVGMIAPASSSTRY 60
QY 61 NQKFKDRFTISVDKSKNTLYLQNSLRAEDTAVYVCARGIYFYGTT--YFDYWGQGTTLVT 118
Db 61 NQKFKDRFTISVDKSKNTLYLQNSLRAEDTAVYVCARGIYFYGTT--YFDYWGQGTTLVT 118
QY 119 VSS 121
Db 120 VSS 122
Search completed: April 13, 2006, 17:20:46
Job time : 36.4017 secs

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OM protein - protein search, using sw model

Run on: April 13, 2006, 17:05:24 ; Search time 246.227 Seconds
(without alignments)
215.918 Million cell updates/sec

Title: US-10-727-737-17

Perfect score: 649

Sequence: 1 EYQLVESGGLVQPGGSLRL.....FYGTTTFDYWGQTLVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 649 | 100.0 | 121 | 2 AAW62019 | Aaw62019 Rhesuise |
| 2 | 649 | 100.0 | 121 | 2 AAW63542 | Aaw63542 Murine MH |
| 3 | 649 | 100.0 | 121 | 3 AAY82348 | Aay82348 Rhesuise |
| 4 | 649 | 100.0 | 121 | 8 ADG39012 | Adg39012 Rhesuise |
| 5 | 649 | 100.0 | 121 | 8 ADR03380 | Adr03380 Rhesuise |
| 6 | 632 | 97.4 | 121 | 2 AAW62013 | Aaw62013 Heavy cha |
| 7 | 632 | 97.4 | 121 | 2 AAW63532 | Aaw63532 Humanised |
| 8 | 632 | 97.4 | 121 | 3 AAY82336 | Aay82336 Humanised |
| 9 | 632 | 97.4 | 121 | 8 ADG38993 | Adg38993 Humanised |
| 10 | 632 | 97.4 | 121 | 8 ADR03368 | Adr03368 Humanised |
| 11 | 632 | 97.4 | 121 | 8 ADR38458 | Adr38458 CD11a hea |
| 12 | 632 | 97.4 | 121 | 9 ADX80646 | Adx80646 Humanized |
| 13 | 632 | 97.4 | 121 | 8 ADF11670 | Adf11670 anti-CD11 |
| 14 | 548.5 | 84.5 | 116 | 2 AAY29452 | Aay29452 Human IGG |
| 15 | 548.5 | 84.5 | 116 | 3 AAY77755 | Aay77755 Human IGG |
| 16 | 548.5 | 84.5 | 116 | 3 AAB30312 | Aab30312 Human IGG |
| 17 | 548.5 | 84.5 | 116 | 6 ABUI3789 | Abui3789 Human IGG |
| 18 | 548.5 | 84.5 | 116 | 6 ABUS5902 | Abu5902 Human IGG |
| 19 | 548.5 | 84.5 | 116 | 7 AAE39085 | Aae39085 Human IGG |
| 20 | 520.5 | 80.2 | 122 | 2 AAR30772 | Aar30772 huxCD3v9, |
| 21 | 516.5 | 79.6 | 122 | 8 ADP79574 | Adp79574 Humanised |
| 22 | 516.5 | 79.6 | 122 | 8 ADS33302 | Ads33302 Anti-CD20 |
| 23 | 516.5 | 79.6 | 122 | 8 ADW03408 | Adw03408 Humanized |
| 24 | 516.5 | 79.6 | 122 | 9 ADW21310 | Adw21310 Mouse ant |

RESULT 1

AAW62019

ID AAW62019 standard; peptide; 121 AA.

XX AC AAW62019;

XX DT 01-OCT-1998 (first entry)

XX DE Rhesuised heavy chain of humanised anti-CD11a antibody.

XX KW Complementarity determining region; heavy chain variable region;

XX KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;

XX KW human CD11a I domain; MHM24 epitope; alpha subunit;

XX KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;

XX KW in vivo imaging; diagnosis; CD11a-associated disease.

XX OS Unidentified.

XX PN WO9823761-A1.

XX PD 04-JUN-1998.

XX PF 20-OCT-1997; 97WO-US019041.

XX PR 27-NOV-1996; 96US-00757205.

XX PA (GETH) GENENTECH INC.

XX XX Jardieu PM, Presta LG;

XX PI WPI; 1998-322737/28.

XX DR New humanised anti-CD11a antibody - used in immunoassays for CD11a, and

XX PT also to treat conditions such as immunological or inflammatory disease.

XX XX Disclosure; Page 56; 66pp; English.

XX CC The present sequence represents the heavy chain of a "rhesuised" (sic)

XX CC humanised anti-CD11a antibody that binds specifically to the human CD11a

XX CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte

XX CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti

XX CC -CD11a antibodies are used to determine presence of CD11a in usual

XX CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-

XX CC associated diseases (typically immune responses and inflammation such as

XX CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,

XX CC leukaemia, etc

XX XX

ALIGNMENTS

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 25 | 516.5 | 79.6 | 122 | 9 | ADX00803 | Adx00803 Humanized |
| 26 | 516.5 | 79.6 | 122 | 9 | ADY62623 | Ady62623 Humanized |
| 27 | 516.5 | 79.6 | 122 | 9 | AEB27726 | Aeb27726 Humanized |
| 28 | 516.5 | 79.6 | 122 | 9 | AEB17636 | Aeb17636 Variable |
| 29 | 516.5 | 79.6 | 452 | 8 | ADS33304 | Ads33304 Anti-CD20 |
| 30 | 516.5 | 79.6 | 452 | 9 | ADM03410 | Adm03410 Humanized |
| 31 | 516.5 | 79.6 | 452 | 9 | ADM03411 | Adm03411 Humanized |
| 32 | 516.5 | 79.6 | 452 | 9 | AEB27728 | Aeb27728 Humanized |
| 33 | 516.5 | 79.6 | 452 | 9 | AEB17638 | Aeb17638 Heavy Cha |
| 34 | 516.5 | 79.6 | 471 | 8 | ADP79584 | Adp79584 2H7.v16 H |
| 35 | 516.5 | 79.6 | 471 | 8 | ADP79585 | Adp79585 2H7.v31 L |
| 36 | 516.5 | 79.6 | 471 | 9 | ADM03399 | Adm03399 Human ant |
| 37 | 516.5 | 79.6 | 471 | 9 | ADM03406 | Adm03406 Human ant |
| 38 | 516.5 | 79.6 | 471 | 9 | ADM21319 | Adm21319 Mouse ant |
| 39 | 516.5 | 79.6 | 471 | 9 | ADM21320 | Adm21320 Mouse ant |
| 40 | 516.5 | 79.6 | 471 | 9 | ADY00805 | Ady00805 Humanized |
| 41 | 516.5 | 79.6 | 471 | 9 | ADY62625 | Ady62625 Humanized |
| 42 | 512.5 | 79.0 | 253 | 2 | RAY29444 | Aay29444 Humanised |
| 43 | 512.5 | 79.0 | 253 | 2 | RAY29454 | Aay29454 Humanised |
| 44 | 512.5 | 79.0 | 253 | 3 | RAY77757 | Aay77757 Humanised |
| 45 | 512.5 | 79.0 | 253 | 3 | RAY77759 | Aay77759 Humanised |

SQ Sequence 121 AA;
 Query Match 100.0%; Score 649; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWGMIAPASSSTRY 60
 |||||
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWGMIAPASSSTRY 60
 |||||

QY 61 NQKFKDRFTTISVDKSKNTLYLQNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTVS 120
 |||||
 Db 61 NQKFKDRFTTISVDKSKNTLYLQNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTVS 120
 |||||

QY 121 S 121
 |
 Db 121 S 121

RESULT 2
 AAW63542
 ID AAW63542 standard; protein; 121 AA.
 XX AAW63542;
 AC
 DT 06-OCT-1998 (first entry)
 XX Murine M24 heavy chain variable domain mutant.
 DE
 XX Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; heavy chain.
 XX
 XX Synthetic.
 OS Mus sp.
 XX WO9823746-A1.
 XX
 XX 04-JUN-1998.
 PD
 XX 29-OCT-1997; 97WO-US020169.
 XX
 XX 27-NOV-1996; 96US-00756150.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Jardieu PM, Presta LG;
 PI
 XX WPI; 1998-322726/28.
 XX
 XX Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 XX Claim 13; Page 59-60; 71pp; English.
 PS
 XX This sequence represents the heavy chain variable domain of a mutant
 CC murine antibody M24 of the invention. The mutants are of a species-
 CC dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced

CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 XX
 SQ Sequence 121 AA;
 Query Match 100.0%; Score 649; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWGMIAPASSSTRY 60
 |||||
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWGMIAPASSSTRY 60
 |||||

QY 61 NQKFKDRFTTISVDKSKNTLYLQNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTVS 120
 |||||
 Db 61 NQKFKDRFTTISVDKSKNTLYLQNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTVS 120
 |||||

QY 121 S 121
 |
 Db 121 S 121

RESULT 3
 AAY82348
 ID AAY82348 standard; protein; 121 AA.
 XX AAY82348;
 AC
 XX AAY82348;
 DT 22-JUN-2000 (first entry)
 XX Rhesusised antibody mutant heavy chain SEQ ID NO:24.
 DE
 XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 KW antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.
 XX
 XX Macaca mulatta.
 OS Mus sp.
 XX US6037454-A.
 XX
 XX 14-MAR-2000.
 PD
 XX 20-NOV-1997; 97US-00974899.
 XX
 XX 27-NOV-1996; 96US-0031971P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Jardieu PM, Presta LG;
 PI
 XX WPI; 2000-282241/24.
 XX
 XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarity determining regions.
 XX
 XX Example; Fig 1; 38pp; English.
 PS
 XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs

CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the amino acid sequence of a rhesusised antibody
 CC mutant heavy chain, which is used in the exemplification of the present
 CC invention

XX Sequence 121 AA;

Query Match 100.0%; Score 649; DB 3; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKLEWGMIAPASSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKLEWGMIAPASSTRY 60
 QY 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVYVCARGIYFYGTTFDYWGQGLTVTVS 120
 DB 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVYVCARGIYFYGTTFDYWGQGLTVTVS 120

CY 121 S 121
 EB 121 S 121

RESULT 4
 ADG39012
 ID ADG39012 standard; protein; 121 AA.

XX ADG39012;

XX 26-FEB-2004 (first entry)

XX Rhesusised mouse anti-CD11a I-domain antibody VL.

XX Mouse; CD11a; I-domain; monoclonal antibody;
 XX cluster of differentiation 11a; mixed lymphocyte response assay;
 XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 XX diabetes mellitus; prodrug activating enzyme.

XX Synthetic.

XX Mus sp.

XX US2003207336-A1.

XX 06-NOV-2003.

XX 28-FEB-2001; 2001US-00795798.

XX 27-NOV-1996; 96US-0031971P.

XX 20-NOV-1997; 97US-00974899.

XX 20-OCT-1999; 99US-00420745.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 2004-051511/05.

XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
 XX associated antigen mediated disorder e.g. psoriasis, Crohns disease,
 XX ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Example; SEQ ID NO 24; 43pp; English.

XX

CC The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the light chain of a rhesusised anti-CD11a antibody of
 CC the invention.

XX Sequence 121 AA;

Query Match 100.0%; Score 649; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKLEWGMIAPASSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKLEWGMIAPASSTRY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVYVCARGIYFYGTTFDYWGQGLTVTVS 120
 DB 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVYVCARGIYFYGTTFDYWGQGLTVTVS 120

CY 121 S 121
 DB 121 S 121

RESULT 5

ADRO3380
 ID ADRO3380 standard; protein; 121 AA.

XX ADRO3380;

XX 21-OCT-2004 (first entry)

XX Rhesusised MHM24 antibody variable heavy chain mutant protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; psoriasis;
 XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
 XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 XX tuberculosis; sarcoidosis; polymyositis;
 XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 XX skin hypersensitivity disorder; poison ivy; poison oak;
 XX B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 XX graft versus host disease; cancer; gene therapy;
 XX murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 XX VH; murine; rhesus macaque; fusion protein; mutant; mutein.

XX Mus sp.

XX Macaca mulatta.

XX Chimeric.

XX US2004146507-A1.

XX 29-JUL-2004.

XX 03-DEC-2003; 2003US-00727737.

XX

PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 PA (GETH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 XX WPI; 2004-552640/53.
 XX
 XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 XX Example; SEQ ID NO 17; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is rhesusised murine anti-human CD11a monoclonal
 CC antibody (MHM24) variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 121 AA;
 Query Match 100.0%; Score 649; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWVGMIAPASSSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWVGMIAPASSSTRY 60
 QY 61 NQKPKDRFTTISVDKSKNTLYLQWNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTS 120
 DB 61 NQKPKDRFTTISVDKSKNTLYLQWNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTS 120
 QY 121 S 121
 DB 121 S 121
 RESULT 6
 AAW62013
 ID AAW62013 standard; peptide; 121 AA.
 XX
 AC AAW62013;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Heavy chain variable region of humanised anti-CD11a antibody.
 XX
 KW Complementarity determining region; heavy chain variable region;
 KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
 KW human CD11a I domain; MHM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO9823761-A1.
 XX

PD 04-JUN-1998.
 XX 20-OCT-1997; 97WO-US019041.
 XX 27-NOV-1996; 96US-00757205.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 XX WPI; 1998-322737/28.
 XX
 XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 XX also to treat conditions such as immunological or inflammatory disease.
 XX
 XX Claim 7; Page 50; 66pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of a
 CC humanised anti-CD11a antibody that binds specifically to the human CD11a
 CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
 CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC CD11a antibodies are used to determine presence of CD11a in usual
 CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
 CC leukaemia, etc
 XX
 SQ Sequence 121 AA;
 Query Match 97.4%; Score 632; DB 2; Length 121;
 Best Local Similarity 96.7%; Pred. No. 5.4e-48;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWVGMIAPASSSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWVGMIHPDSETRY 60
 QY 61 NQKPKDRFTTISVDKSKNTLYLQWNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTS 120
 DB 61 NQKPKDRFTTISVDKSKNTLYLQWNSLRAEDTAVYVCARGIFYGTTTFDYWGQGLTVTS 120
 QY 121 S 121
 DB 121 S 121
 RESULT 7
 AAW63532
 ID AAW63532 standard; protein; 121 AA.
 XX
 AC AAW63532;
 XX
 DT 06-OCT-1998 (first entry)
 XX
 DE Humanised MHM24 heavy chain.
 XX
 KW Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; heavy chain.
 XX
 OS Synthetic.
 XX
 PN WO9823746-A1.
 XX
 PD 04-JUN-1998.
 XX
 XX 29-OCT-1997; 97WO-US020169.
 XX
 XX 27-NOV-1996; 96US-00756150.
 XX
 XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;
 XX MPI; 1998-322726/28.
 XX Mutants of species-dependent antibodies with affinity for non-human
 XX mammalian antigen - greater than for parent antibody, particularly used
 XX for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 XX directed against CD11a.
 XX Disclosure; Page 55; 71pp; English.
 XX This sequence represents the heavy chain of the humanised antibody MEM24,
 XX and was used to produce a mutant of the invention. The mutants are of a
 XX species-dependent antibody (Ab), and have an amino acid substitution in a
 XX variable region of the Ab, and binding affinity for an antigen (Ag) from
 XX a non-human mammal at least 10 times stronger than for the wild type Ab
 XX against the Ag. The mutant antibodies are particularly intended for
 XX administration to a non-human mammal in preclinical studies (e.g. of
 XX infection, immunity, haematopoiesis or transplantation). They can also be
 XX used diagnostically (to identify specific proteins) or therapeutically,
 XX e.g. where directed against CD11a (lymphocyte function-associated antigen
 XX -1) or intercellular adhesion molecule-1 against a wide variety of
 XX inflammatory or autoimmune diseases, malignancies, transplant rejection,
 XX human immune deficiency virus infection and tumour cell invasion.
 XX Conversion to the mutant form allows useful antibodies to be produced
 XX from antibodies which normally have affinity for non-human analogues of
 XX the Ag too low to be of any use
 XX Sequence 121 AA;
 SQ
 Query Match 97.4%; Score 632; DB 2; Length 121;
 Best Local Similarity 96.7%; Pred. No. 5.4e-48;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVGVGMIAPASSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVGVGMIAHPSDSTRY 60
 QY 61 NQPKDRFTTISVDKSKNTLYLQNSLRADTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 DB 61 NQPKDRFTTISVDKSKNTLYLQNSLRADTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 QY 121 S 121
 DB 121 S 121
 RESULT 8
 ID AAY82336
 AC AAY82336;
 XX 22-JUN-2000 (first entry)
 XX Humanised anti-CD11a antibody heavy chain variable region SEQ ID NO:5.
 XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 XX antitumour; antiviral; inflammation; immunological response; LFA-1;
 XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 XX viral infection; transplant rejection; graft rejection.
 XX Homo sapiens.
 OS Mus sp.
 XX US6037454-A.
 XX 14-MAR-2000.
 XX 20-NOV-1997; 97US-00974899.
 XX

PR 27-NOV-1996; 96US-0031971P.
 PA (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 PI MPI; 2000-282241/24.
 DR New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 XX inflammation and transplant rejection, contains human heavy variable
 XX region complementarity determining regions.
 XX Claim 1; Fig 1; 38pp; English.
 XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 XX binds specifically to the human CD11a I-domain. The Ab has anti-
 XX inflammatory, immunosuppressant, antitumour and antiviral activities. The
 XX Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 XX involved in leucocyte adhesion associated with inflammatory and
 XX immunological responses. The Ab are used: (i) optionally when coupled to
 XX a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 XX function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 XX inflammatory bowel disease, eczema, systemic lupus erythematosus,
 XX rhinitis, leukaemia, viral infections and many others, also for
 XX inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 XX tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 XX to active anticancer agent; and (v) for affinity chromatography. The Ab
 XX retain about the same activity in adhesion and mixed lymphocyte response
 XX assays as the murine antibodies from which they are derived. The murine
 XX anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
 XX between Jurkat cells (expressing LFA-1) and normal epidermal
 XX keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 XX The fully humanized version of MEM24 had IC50 0.13 nM. The present
 XX sequence represents the heavy chain variable region of the humanised anti
 XX -CD11a Ab
 XX Sequence 121 AA;
 SQ
 Query Match 97.4%; Score 632; DB 3; Length 121;
 Best Local Similarity 96.7%; Pred. No. 5.4e-48;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVGVGMIAPASSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVGVGMIAHPSDSTRY 60
 QY 61 NQPKDRFTTISVDKSKNTLYLQNSLRADTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 DB 61 NQPKDRFTTISVDKSKNTLYLQNSLRADTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 QY 121 S 121
 DB 121 S 121
 RESULT 9
 ID ADG38993
 AC ADG38993 standard; protein; 121 AA.
 XX ADG38993;
 XX 26-FEB-2004 (first entry)
 XX Humanised Mouse anti-CD11a antibody heavy chain variable region.
 XX Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
 XX VH; cluster of differentiation 11a; mixed lymphocyte response assay;
 XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 XX diabetes mellitus; prodrug activating enzyme; humanised.
 XX

OS Synthetic.
 OS Mus sp.
 PN US2003207336-A1.
 XX 06-NOV-2003.
 PD
 XX
 XX 28-FEB-2001; 2001US-00795798.
 XX
 XX 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 PI WPI; 2004-051511/05.
 DR
 XX
 XX Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohns disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 PT
 PT
 XX
 PS Claim 7; SEQ ID NO 5; 43pp; English.
 XX
 XX The invention relates to a Humanised anti-cluster of differentiation (CD)11a antibody having specificity to human CD11a I-domain or CD11a with a kd value of not more than 1x10⁻⁸ M, or concentration for 50 % inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM) -1. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The antibody is useful for determining the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the heavy chain variable region (VH) of the humanised mouse anti-CD11a I domain monoclonal antibody MHM24.
 XX
 XX Sequence 121 AA;
 Query Match 97.4%; Score 632; DB 8; Length 121;
 Best Local Similarity 96.7%; Pred. No. 5.4e-48;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWGMIAHPSDSSTRY 60
 QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRADPAVYVCARGIFYGTTTFDYWGQGTILVTVS 120
 Db 61 NQKFKDRFTISVDKSKNTLYLQMSLRADPAVYVCARGIFYGTTTFDYWGQGTILVTVS 120
 QY 121 S 121
 Db 121 S 121
 RESULT 10
 ID ADR03368
 XX ADR03368 standard; protein; 121 AA.
 AC ADR03368;
 XX
 XX 21-OCT-2004 (first entry)
 XX
 XX Humanised MHM24 F(ab)-8 antibody variable heavy chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection; rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; adult respiratory distress syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SLE; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak; hairy cell leukaemia; B-cell malignancy; chronic lymphocytic leukaemia; cancer; gene therapy; graft versus host disease; cancer; murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain; VH; murine; human; fusion protein.
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX US2004146507-A1.
 XX 29-JUL-2004.
 PD
 XX 03-DEC-2003; 2003US-00727737.
 XX
 XX 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 PI WPI; 2004-552640/53.
 DR
 XX New antibody mutant of a species-dependent antibody, useful for treating and preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
 PS Example; SEQ ID NO 5; 54pp; English.
 XX The present invention relates to an antibody mutant of a species-dependent antibody with beneficial properties. The invention is useful for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD11a monoclonal antibody (MHM24) F(ab)-8 variable heavy chain protein. This sequence is used in the exemplification of the invention.
 CC
 CC Sequence 121 AA;
 Query Match 97.4%; Score 632; DB 8; Length 121;
 Best Local Similarity 96.7%; Pred. No. 5.4e-48;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKLEWGMIAHPSDSSTRY 60
 QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRADPAVYVCARGIFYGTTTFDYWGQGTILVTVS 120
 Db 61 NQKFKDRFTISVDKSKNTLYLQMSLRADPAVYVCARGIFYGTTTFDYWGQGTILVTVS 120
 QY 121 S 121

KW high-performance tangential flow filtration; HPTFF; pharmaceutical;
 KW diagnostic; therapeutic; antibody.
 OS Synthetic.
 XX WO2003102132-A2.
 XX 11-DEC-2003.
 XX 25-APR-2003; 2003WO-US013054.
 XX 26-APR-2002; 2002US-0375953P.
 XX (GETH) GENENTECH INC.
 XX Fahner RL, Follman D, Lebreton B, Van Reis R;
 XX WPI; 2004-043096/04.
 XX Purifying target protein from mixture containing host cell protein
 PT involves subjecting mixture to non-affinity purification, high-
 PT performance tangential flow filtration and isolating purified protein.
 XX Disclosure; SEQ ID NO 4; 77pp; English.
 XX The invention relates to a method for purifying a target protein from a
 CC mixture containing a host cell protein. This method comprises subjecting
 CC the mixture to a non-affinity purification followed by high-performance
 CC tangential flow filtration (HPTFF) and isolating the protein in a purity
 CC containing less than 100 parts/million (ppm) of the host cell protein,
 CC where the method of the invention includes no affinity purification
 CC process. The method of the invention is useful for purifying a target
 CC protein from a mixture containing a host cell protein, and is useful for
 CC incorporating the isolated protein into a pharmaceutical formulation.
 CC proteins purified using the method of the invention are useful in a
 CC pharmaceutical respect, and are also useful in various diagnostic and
 CC therapeutic purposes. The method of the invention is efficient in
 CC purifying a target protein from a mixture containing a host cell protein,
 CC and may also be effectively performed at low cost. The current sequence
 CC represents the anti-CD11a rhWAB heavy chain amino acid sequence. This
 CC particular protein was used to demonstrate the method of the invention.
 XX
 SQ Sequence 451 AA;
 Query Match 97.4%; Score 632; DB 8; Length 451;
 Best Local Similarity 96.7%; Pred. No. 2.1e-47;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHNNWVRQAPGKLEWVGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHNNWVRQAPGKLEWVGMIHPSDSETRY 60
 Qy 61 NQPKDRFTTSVDKSKNTLYLQNNLSRAEDTAVYCYARGIFYGTTFYDWGQGLTVTS 120
 Db 61 NQPKDRFTTSVDKSKNTLYLQNNLSRAEDTAVYCYARGIFYGTTFYDWGQGLTVTS 120
 Qy 121 S 121
 Db 121 S 121
 RESULT 14
 AAY29452
 ID AAY29452 standard; protein; 116 AA.
 XX
 AC AAY29452;
 XX
 XX 05-OCT-1999 (first entry)
 XX Human IgG1 subgroup III heavy chain variable domain.
 XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
 KW diagnosis; inflammatory disorder; conjugate; immunoglobulin;
 XX

KW fusion protein.
 XX Homo sapiens.
 XX WO9937779-A1.
 XX 29-JUL-1999.
 XX 19-JAN-1999; 99WO-US001081.
 XX 22-JAN-1998; 98US-00012116.
 XX 20-FEB-1998; 98WO-US003337.
 XX 24-JUL-1998; 98US-00121952.
 XX 24-JUL-1998; 98US-00122513.
 XX (GETH) GENENTECH INC.
 XX Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
 XX WPI; 1999-469134/39.
 XX New conjugates of nonproteinaceous polymers with antibody fragments, used
 PT for treating inflammatory disorders.
 XX Disclosure; Fig 29; 360pp; English.
 XX The present invention describes a novel conjugate having one or more
 CC antibody fragments covalently attached to one or more nonproteinaceous
 CC polymer molecules, where the apparent size of the conjugate is at least
 CC about 500 kDa. Conjugates of antibody fragments which bind the human
 CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
 CC treating inflammatory disorders e.g. acute lung injury, ischaemic
 CC reperfusion disorder, and autoimmune diseases. They can also be used for
 CC treating e.g. inflammatory skin diseases including psoriasis and atopic
 CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.
 CC The conjugates can also be used as reagents in an animal model system for
 CC in vivo study of the biological functions of the antigen recognised by
 CC the conjugate. The present sequence represents the human IgG1 subgroup
 CC III heavy chain variable domain form the present invention
 XX
 SQ Sequence 116 AA;
 Query Match 84.5%; Score 548.5; DB 2; Length 116;
 Best Local Similarity 88.8%; Pred. No. 1.2e-40;
 Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHNNWVRQAPGKLEWVGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHNNWVRQAPGKLEWVGMIHPSDSETRY 60
 Qy 61 NQPKDRFTTSVDKSKNTLYLQNNLSRAEDTAVYCYARGIFYGTTFYDWGQGLTVTS 115
 Db 61 ADSVKGRFTTSRDNSKNTLYLQNNLSRAEDTAVYCYAARGIFYGTTFYDWGQGLTVTS 116
 RESULT 15
 AAY77755
 ID AAY77755 standard; protein; 116 AA.
 XX
 AC AAY77755;
 XX
 XX 06-JUN-2000 (first entry)
 XX Human IgG1 subgroup III heavy chain variable domain.
 XX Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.5V11N35A;
 KW inflammatory disorder; adult respiratory distress syndrome; chimeric;
 KW affinity purification; 6G4.2.5.
 XX Homo sapiens.
 XX US6025158-A.
 XX

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OM protein - protein search, using sw model

Run on: April 13, 2006, 17:14:06 ; Search time 25.8908 Seconds
(without alignments)
449.666 Million cell updates/sec

Title: US-10-727-737-17
Perfect score: 649
Sequence: 1 EVQLVESGGLVQPGGSLRL.....FYGTTTFDYWGQGTLLTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 461 | 71.0 | 125 | S30531 | Ig heavy chain V r |
| 2 | 461 | 71.0 | 140 | S31686 | Ig heavy chain V r |
| 3 | 460.5 | 71.0 | 140 | S70442 | Ig heavy chain pre |
| 4 | 459 | 70.7 | 140 | S31588 | Ig heavy chain V r |
| 5 | 457.5 | 70.5 | 128 | S26786 | Ig heavy chain V r |
| 6 | 457 | 70.4 | 121 | S26798 | Ig heavy chain V r |
| 7 | 455 | 70.1 | 119 | S31107 | Ig heavy chain - h |
| 8 | 454 | 70.0 | 119 | S31108 | Ig heavy chain - h |
| 9 | 452.5 | 69.7 | 124 | S20782 | Ig heavy chain V r |
| 10 | 451 | 69.5 | 143 | S23624 | Ig heavy chain V r |
| 11 | 450.5 | 69.4 | 141 | S31669 | Ig heavy chain V r |
| 12 | 450 | 69.3 | 123 | S26794 | Ig heavy chain V r |
| 13 | 449.5 | 69.3 | 120 | S48798 | Ig heavy chain V r |
| 14 | 448 | 69.0 | 121 | S19666 | Ig heavy chain V r |
| 15 | 447.5 | 69.0 | 136 | S31587 | Ig heavy chain V r |
| 16 | 447 | 68.9 | 120 | S36273 | Ig heavy chain V r |
| 17 | 446.5 | 68.8 | 147 | S13780 | Ig variable region |
| 18 | 446 | 68.7 | 121 | S55673 | Ig heavy chain - h |
| 19 | 446 | 68.7 | 123 | S31114 | Ig heavy chain - h |
| 20 | 443 | 68.3 | 119 | S36005 | Ig heavy chain V r |
| 21 | 443 | 68.3 | 121 | S36005 | Ig heavy chain V r |
| 22 | 443 | 68.3 | 132 | S31603 | Ig heavy chain V r |
| 23 | 443 | 68.3 | 138 | S31666 | Ig heavy chain V r |
| 24 | 442.5 | 68.2 | 119 | AVMSX4 | Ig heavy chain V r |
| 25 | 442 | 68.1 | 117 | S31109 | Ig heavy chain - h |
| 26 | 442 | 68.1 | 160 | S05271 | Ig heavy chain pre |
| 27 | 441 | 68.0 | 117 | S78486 | Ig heavy chain V r |
| 28 | 439 | 67.6 | 118 | S47329 | Ig heavy chain V r |
| 29 | 439 | 67.6 | 119 | D36005 | Ig heavy chain V r |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 438.5 | 67.6 | 136 | 2 | S13791 | Ig heavy chain V r |
| 31 | 438 | 67.5 | 120 | 2 | S36278 | Ig heavy chain V r |
| 32 | 437.5 | 67.4 | 114 | 2 | S31120 | Ig heavy chain - h |
| 33 | 437.5 | 67.4 | 119 | 1 | AVMST6 | Ig heavy chain V r |
| 34 | 436 | 67.2 | 121 | 2 | H36005 | Ig heavy chain V r |
| 35 | 435.5 | 67.1 | 128 | 2 | S26790 | Ig heavy chain V r |
| 36 | 435 | 67.0 | 127 | 2 | S38489 | Ig heavy chain - h |
| 37 | 435 | 67.0 | 135 | 2 | S31598 | Ig heavy chain V r |
| 38 | 434 | 66.9 | 130 | 2 | S31601 | Ig heavy chain V r |
| 39 | 433.5 | 66.8 | 119 | 1 | AVMSJ5 | Ig heavy chain V r |
| 40 | 433.5 | 66.8 | 122 | 2 | S20772 | Ig heavy chain V r |
| 41 | 433 | 66.7 | 117 | 2 | S34012 | Ig heavy chain V r |
| 42 | 433 | 66.7 | 139 | 2 | A25912 | Ig heavy chain pre |
| 43 | 432 | 66.6 | 134 | 2 | S31699 | Ig heavy chain V r |
| 44 | 431.5 | 66.5 | 120 | 2 | S44111 | Ig heavy chain V-D |
| 45 | 431.5 | 66.5 | 122 | 2 | S31117 | Ig heavy chain - h |

ALIGNMENTS

RESULT 1

S30531
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C;Accession: S30531
R;Marette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <MAR>
A;Cross-references: UNIPROT:Q9UL91; UNIPARC:UPI0000176C10; EMBL:Z18317
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 461; DB 2; Length 125;
Best Local Similarity 72.0%; Pred. No. 5.6e-36;
Matches 90; Conservative 12; Mismatches 19; Indels 4; Gaps 1;
Qy 1 EVQLVESGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPFGKLEWVGMTPAPSSSTRY 60
Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTSSYMNWVRQAPFGKLEWISYSSSSSTIY 60
Qy 61 NQKPKDRFTTSVDKSKVTLVQNNSLRAEDTAVVYCARGIYF----YGTTFDYWGQGT 116
Db 61 ADSVKGRTTISRDNKNSLYLQNNSLRAEDTAVVYCARSRNYDSGGYSHYFDYWGQGT 120
Qy 117 VTVSS 121
Db 121 VTVSS 125

RESULT 2

S31686
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31686
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPARC:UPI0000116477; EMBL:Z14205; NID:G30969; PIDN:CAA78574.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

| | | | | | | | |
|-----------------------|-------|--------------|----------|------------|-----|--------|------|
| Query Match | 71.0% | Score | 461; | DB | 2; | Length | 140; |
| Best Local Similarity | 73.6% | Pred. No. | 6.3e-36; | | | | |
| Matches | 89; | Conservative | 12; | Mismatches | 20; | Indels | 0; |
| Gaps | 0; | | | | | | |

| | | | | |
|----|-----|---|------------|-----|
| Qy | 1 | EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWQAQPKGLEWGMIA | PASSSTRY | 60 |
| | | | | |
| Db | 20 | EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWRQAQPKGLEWVSA | ISGGGGSTYY | 79 |
| | | | | |
| | | | | |
| Qy | 61 | NQKFKDRFTISVDKSKNTLYLQMSLRADTAVVYCYFGTYTPDYWGQGT | LTIVTS | 120 |
| | | | | |
| | | | | |
| Db | 80 | SDSVKGRFTISRDNSKNTLYLQMSLRADTAVVYCAKCPAGGSPSDYWGQGT | LTIVTS | 139 |
| | | | | |
| Qy | 121 | S | 121 | |
| | | | | |
| Db | 140 | S | 140 | |

```

RESULT 3
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
C/Accession: S70442
R/Cuisinier, A.M.; Funoux, P.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: tGM kappa/lambda BBV human B cell clone: an early step of differentiation of fe
A/Reference number: S70442; MUID:93024508; PMID:1383695
A/Accession: S70442
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI00000176EB7
C/Superfamily: immunoglobulin homology
P/34-117/Domain: immunoglobulin homology <IMW>

```

| | | | | | | | |
|-----------------------|--------|--------------|------------|------------|-----|--------|------------|
| Query Match | 71.0%; | Score | 460.5; | DB | 2; | Length | 140; |
| Best Local Similarity | 74.4%; | Pred. | No. 7e-36; | | | | |
| Matches | 90; | Conservative | 9; | Mismatches | 21; | Indels | 1; Gaps 1; |

| | | | | | | |
|----|-----|---------------|------------|---------------------------|---------------------|-----|
| Qy | 1 | EVLVESGGGIVQP | GGSIRLS | CAASGVSYFTCHWNNVWRQA | PKGLEWVGMTAPASSSTRY | 60 |
| | : | : : | : | : | : | : |
| Dd | 20 | QVQLVESGGGVVP | QGSSIRLRS | CAASGTFSTFSGYHMHVWRQA | PKGLEWVAFYR | 79 |
| | : | : : | : | : | : | : |
| Qy | 61 | NQRPFKDRFTTIS | VDKSKNTLYL | QNMSLRADPTAVYYCARGI | FYGYGTTFDYWGQGLTVTS | 120 |
| | : | : | : | : | : | : |
| Dd | 80 | ADSVKGRTFTSRD | NSKNTLYL | QNMSLRADPTAVYYCARD-HIVGAT | FDYWGQGLTVTS | 138 |
| | : | : | : | : | : | : |
| Qy | 121 | S | 121 | | | |
| | | | | | | |
| Dd | 139 | S | 139 | | | |

RESULT 4

S31588

IG heavy chain V region - human (fragment)

C1:Species: Homo sapiens (man)

C2:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C3:Accession: S31588

R:Guissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A:submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31588

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: UNIPARC:UPI0000116472; EMBL:Z14200; NID:g30957; PID:CAA78569.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

```

Query Match          70.7%; Score 459; DB 2; Length 140;
Best Local Similarity 73.6%; Pred. NO. 9.6e-36;
Matches 89; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLCSAASGYSFTGHMMHWVRQAPGKGLEWVGMIAPASSTRY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20 EVQLLESGGGLVQPGGSLRLCSAASGPTFSYAMSWVRQAPGKGLEWVAISGGSGSTYY 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 NQKFKDRPTISVDKSKNTLYLQMSLSRAEDTAVVYCARGIYFVGITYFDYWGQGLTLVTVS 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80 ADSVKGRPTISDRDSKNTLYLQMSLSRAEDTAVVYCAKDHYSNYIFYDWGQGLTLVTVS 139
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 S 121
      |
Db      140 S 140

RESULT 5
S26786
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26786
R:Mortari, P.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26786
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <MOR>
A:Cross-references: UNIPARC:UPI0000115FC5; EMBL:X61014; NID:G32800; PIDN:CAA43348.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

RESULT 5

S26786

19 heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26786

R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family

A:Reference number: S26786; MUID:92111632; PMID:1730251

A:Accession: S26786

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <MOR>

A:Cross-references: UNIPARC:UPI0000115FC5; EMBL:X61014; NID:G32800; PIDN:CAA43348.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

```

Query Match          70.5%; Score 457.5; DB 2; Length 128;
Best Local Similarity 68.0%; Pred. NO. 1.2e-35;
Matches 87; Conservative 16; Mismatches 18; Indels 7; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWQAPCKGLEWGMIPASSTSY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFTSYIMSWIRQAPCKGLEWYSISSSSY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 NQKFKDFTISVDKSKNTLYLQMNSLRAEDTAVVYCARGI-----YFYGTTYDPYWGQ 113
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGFTISRDNKNSLYLQMNSLRAEDTAVVYCARGLYCSTSYIWSNNWFDPMWQ 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 114 GTLVTVSS 121
   |||||
Db 121 GTLVTVSS 128
   |||||

RESULT 6
S26798
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26798
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26798
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <MOR>
A:Cross-references: UPI0000115FC6; EMBL:X61015; NID:G32795; PIDN:CAA43349.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          70.4%; Score 457; DB 2; Length 121;

```

RESULT 6
S26798
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26798
R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family
A/Reference number: S26786; MUID:92111632; PMID:1730251
A/Accession: S26798
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-121 <MOR>
A/Cross-references: UPT0000115FC6; EMBL:X61015; NID:G32795; PIDN:CAA43349.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 457; DB 2; Length 121;

Query Match 70.4%; Score 457; DB 2; Length 121;

```
Best Local Similarity 71.9%; Pred. No. 1.3e-35;
Matches 87; Conservative 7; Mismatches 27; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQPKDRFTTISVDKSKNTLYLQNNSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 S 121
Db 121 S 121

RESULT 7
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
  Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31107
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <PAA>
A:Cross-references: UNIPARC:UPI0000176DC7; EMBL:X62955
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 455; DB 2; Length 119;
Best Local Similarity 74.0%; Pred. No. 1.9e-35;
Matches 91; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQPKDRFTTISVDKSKNTLYLQNNSLRAEDTAVVYCAR--GIYFYGTTFDYWGQGLTVT 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVVYCARPGASY----YFDYWGQGLTVT 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 VSS 121
Db 117 VSS 119

RESULT 8
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
  Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31108
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <PAA>
A:Cross-references: UNIPARC:UPI0000176DC8; EMBL:X62956
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
```

```
Query Match 70.0%; Score 454; DB 2; Length 119;
Best Local Similarity 74.4%; Pred. No. 2.4e-35;
Matches 90; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQPKDRFTTISVDKSKNTLYLQNNSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVVYCARDKRLTGT--PDYWGQGLTVTS 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 S 121
Db 119 S 119

RESULT 9
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: S20782
R:Mortari, F.; Wang, J.; Schroeder, H.W.
  submitted to the EMBL Data Library, April 1992
A:Description: Analysis of the IGA and IGB rearranged VH repertoire of human cord blood
A:Reference number: S20765
A:Accession: S20782
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <MOR>
A:Cross-references: UNIPARC:UPI00001163EA; EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 452.5; DB 2; Length 124;
Best Local Similarity 72.6%; Pred. No. 3.4e-35;
Matches 90; Conservative 11; Mismatches 20; Indels 3; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFGTHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQPKDRFTTISVDKSKNTLYLQNNSLRAEDTAVVYCAR--GIYFYGTTFDYWGQGLTV 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVVYCARIAIFGVVPHFDYWGQGLTV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 TVSS 121
Db 121 TVSS 124

RESULT 10
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23624
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defcos, M.; Kozin, F.; Carson, D.A.;
  J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23624
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <OLE>
A:Cross-references: UNIPARC:UPI0000115F94; EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 451; DB 2; Length 143;
```

Best Local Similarity 74.4%; Pred. NO. 5.5e-35;
Matches 90; Conservative 9; Mismatches 18; Indels 4; Gaps 1

```
Qy      1 EVQLVESGGGLVQPCCGSRLLSCAASGYSTGHNNWVRQAPEGKLEWGIMTAPASSSTRY 60  
         ||||| :||| |:::| :||||| :||| |:::| :||| |  
Db      1 EVQLVESGGGLVQPCCGSRLLSCAASGFTFSNYSMNWVRQAPEGKLEWSYISSSSTRY 60  
         ||||| :||| |:::| :||||| :||| |:::| :||| |  
  
Qy     61 NQEKDRPTISVDKSKNTLYLQMNSLRADTAIVYFCARGIYFYGTYYDYVGQGTLVTVS 120  
         ||||| :||| |:::| :||||| :||| |:::| :||| |  
Db     61 ADSVKGREPISRDNAKNSLYLQMNSLRADTAIVYFCARSGRGG----DYVGQGTLVTVS 116  
  
Qy    121 S 121  
      |  
Db   117 S 117
```

```

RESULT 11
S31669
lg heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31669
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A:Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31595
A:Accession: S31669
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CUI>
A:Cross-references: UNIPARC:UPI000011647C; EMBL:Z14212; NID:G30959; PIDN:CAA78581.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

```

| | | | | |
|--|-------|---|-------|-------------|
| Query Match | 69.4% | Score 450.5; | DB 2; | Length 141; |
| Best Local Similarity | 73.0% | Fred. NO. 6e-35; | | |
| Matches 89; Conservative 11; Mismatches 21; Indels 1; Gaps 1 | | | | |
| Qy | 1 | EVQLVESGGGLVQPGRSURLSCAASGYSTGHMMNWVRQAQPKGLEWGMITAPASSSTRY | 60 | |
| | | : : : : | | |
| Dd | 20 | EVQLVESGGGLVQPGRSURLSCAASGFTFSYSNMNWRQAQPKGLEWSSISSSSYIYY | 79 | |
| | | : : : : | | |
| Qy | 61 | NQKPKDFTTISVDKSQNTLYLQMNSLRAREDVAIVYCARGIYFYGT-YFDYWGGQTLLVTY | 119 | |
| | | : : : : | | |
| Dd | 80 | ADSVKGRTISRDNAKNSLYLQMNSLRAREDVAIVYCARGHLTGEGKYFDLNGRGLTVY | 139 | |
| | | : : : : | | |
| Qy | 120 | SS 121 | | |
| | | | | |
| Dd | 140 | SS 141 | | |

RESULT 12

S26794

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999

C/Accession: S26794

R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family

A/Reference number: S26786; MUID:92111632; PMID:1730251

A/Accession: S26794

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-123 <MOR>

A/Cross-references: UNIPARC:UPI0000176C2B; EMBL:X61011

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 450; DB 2; Length 123;
Best Local Similarity 71.5%; Pred. No. 5.8e-35;

| | Matches | 88; | Conservative | 11; | Mismatches | 22; | Indels | 2; | Gaps | 1 |
|----|---------|------------------------------------|-----------------------------|-----|------------|-----|--------|----|------|---|
| Qy | 1 | EVQLVGGGGLVQPGGSLRLISCAASGYSTFGHMN | WVRQAPGKGLIEWGMIAPASSSTRY | 60 | | | | | | |
| | | | | : | | : | | : | | |
| Db | 1 | EVQLVGGGGLVQPGGSLRLISCAASGTFSSY | SNMWRQAPGKGLIEWYSIGSSSSSTRY | 60 | | | | | | |
| | | | | : | | : | | : | | |
| Qy | 61 | NQKPKDFTISVDKSKNTLYLQNNLSRAEDTAV | YVCARGIYFYGTTF--DYWGQGTLLVT | 118 | | | | | | |
| | | | | : | | : | | : | | |
| Db | 61 | ADSVKGHTISRDNAKNSLYLQNNLSRDEDTAV | YVCARSIKKYDENYYGMDVWGQGTTVT | 120 | | | | | | |
| | | | | : | | : | | : | | |
| Qy | 119 | VSS | 121 | | | | | | | |
| | | | | | | | | | | |
| Db | 121 | VSS | 123 | | | | | | | |
| | | | | | | | | | | |

```

RESULT 13
S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S48798
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies
A:Reference number: S48797
A:Accession: S48798
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <NAH>
A:Cross-references: UNIPARC:UPI0000116701; EMBL:Z46382; NID:9562324; PIDN:C
S:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

[illegible]

RESULT 14

S19666

Ig heavy chain V region (VH3DJH4) - human

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19666

R:Markes, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, J. Mol. Biol. 222, 581-597, 1991

A:Title: By-passing immunization. Human antibodies from V-gene libraries directed against a protein antigen.

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19666

A:Molecule type: mRNA

A:Residues: 1-121 <MAR>

A:Cross-references: UNIPARC:UPI000011SPF5; EMBL:X61646; NID:g37688; PIDN:CA

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 448; DB 2; Length 121;
Best Local Similarity 71.9%; Pred. No. 8.7e-35;
Matches 87; Conservative 12; Mismatches 22; Indels 0; Gaps 0

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTCHWNNWYRQAPGKLEWVGMIAPASSSTRY 60
 Db 1 QVQLVDSGGGVQPGGSLRLSCAASGYSPTCHWNNWYRQAPGKLEWVGMIAPASSSTRY 60
 QY 61 NQKPKDRTISVDKSKNTLYLQNSLRADTAIVYCARGIYFYGTTFDYWGQGTLLVTVS 120
 Db 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARGIYFYGTTFDYWGQGTLLVTVS 120
 QY 121 S 121
 Db 121 S 121

RESULT 15

S31587
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S31587
 R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
 A;Submitted to the EMBL Data Library, June 1992
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A;Reference number: S31585
 A;Accession: S31587
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-136 <CUI>
 A;Cross-references: UNIPARC:UPI0000116469; EMBL:Z14189; NID:G31005; PIDN:CAA78558.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;31-114/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 447.5; DB 2; Length 136;
 Best Local Similarity 72.7%; Pred. No. 1.1e-34;
 Matches 88; Conservative 9; Mismatches 23; Indels 1; Gaps 1;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTCHWNNWYRQAPGKLEWVGMIAPASSSTRY 60
 Db 17 EVQLVESGGGLVQPGGSLRLSCAASGYSPTCHWNNWYRQAPGKLEWVGMIAPASSSTRY 76
 QY 61 NQKPKDRTISVDKSKNTLYLQNSLRADTAIVYCARGIYFYGTTFDYWGQGTLLVTVS 120
 Db 77 VDSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARGL-TGATDAPDINGQGTLLVTVS 135
 QY 121 S 121
 Db 136 S 136

Search completed: April 13, 2006, 17:19:34
 Job time : 27.8908 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 17:05:54 ; Search time 156.93 Seconds
(without alignments)
543.993 Million cell updates/sec

Title: US-10-727-737-17

Perfect score: 649

Sequence: 1 EVOLVESGGGLVPGQSLRL.....FYGTTYFDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 442.5 | 68.2 | 119 | 1 HV37 MOUSE | P01807 mus musculus |
| 2 | 442.5 | 68.1 | 493 | 2 Q6GMX2 HUMAN | Q6GMX2 homo sapien |
| 3 | 442.5 | 68.1 | 597 | 2 Q96BB9 HUMAN | Q96BB9 homo sapien |
| 4 | 441.5 | 68.0 | 606 | 2 Q6GMV2 HUMAN | Q6GMV2 homo sapien |
| 5 | 438.5 | 67.6 | 467 | 2 Q4VEH1 RAT | Q4VEH1 rattus norv |
| 6 | 437.5 | 67.4 | 119 | 1 HV38 MOUSE | P01808 mus musculus |
| 7 | 436 | 67.2 | 479 | 2 Q5PQK9 RAT | Q5PQK9 rattus norv |
| 8 | 435 | 67.0 | 470 | 2 Q6PJA4 HUMAN | Q6PJA4 homo sapien |
| 9 | 434.5 | 66.9 | 469 | 2 Q569F4 HUMAN | Q569F4 homo sapien |
| 10 | 434 | 66.9 | 478 | 2 Q6P181 HUMAN | Q6P181 homo sapien |
| 11 | 433.5 | 66.8 | 119 | 1 HV40 MOUSE | P01810 mus musculus |
| 12 | 433 | 66.7 | 121 | 2 Q9UL71 HUMAN | Q9UL71 homo sapien |
| 13 | 429 | 66.1 | 113 | 2 Q9UL90 HUMAN | Q9UL90 homo sapien |
| 14 | 428.5 | 66.0 | 118 | 2 Q9UL91 HUMAN | Q9UL91 homo sapien |
| 15 | 428 | 65.9 | 118 | 1 HV39 MOUSE | P01809 mus musculus |
| 16 | 427 | 65.8 | 464 | 2 Q6MZU6 HUMAN | Q6MZU6 homo sapien |
| 17 | 424.5 | 65.4 | 118 | 2 Q9UL72 HUMAN | Q9UL72 homo sapien |
| 18 | 424.5 | 65.4 | 613 | 2 Q8WUK1 HUMAN | Q8WUK1 homo sapien |
| 19 | 422 | 65.0 | 131 | 2 Q9UL88 HUMAN | Q9UL88 homo sapien |
| 20 | 421.5 | 64.9 | 465 | 2 Q6P6C4 HUMAN | Q6P6C4 homo sapien |
| 21 | 421.5 | 64.9 | 473 | 2 Q6MZV7 HUMAN | Q6MZV7 homo sapien |
| 22 | 421 | 64.9 | 240 | 2 Q55ZC9 HUMAN | Q55ZC9 homo sapien |
| 23 | 420.5 | 64.8 | 494 | 2 Q96K68 HUMAN | Q96K68 homo sapien |
| 24 | 419.5 | 64.6 | 139 | 1 HV07 MOUSE | P01751 mus musculus |
| 25 | 419.5 | 64.6 | 145 | 2 Q924Q7 MOUSE | Q924Q7 mus musculus |
| 26 | 418 | 64.4 | 115 | 1 HV3D HUMAN | P01765 homo sapien |
| 27 | 418 | 64.4 | 117 | 1 HV41 MOUSE | P01811 mus musculus |
| 28 | 418 | 64.4 | 479 | 2 Q5BK72 RAT | Q5BK72 rattus norv |
| 29 | 417.5 | 64.3 | 475 | 2 Q6MZQ6 HUMAN | Q6MZQ6 homo sapien |
| 30 | 417 | 64.3 | 146 | 2 Q924Q3 MOUSE | Q924Q3 mus musculus |
| 31 | 417 | 64.3 | 472 | 2 Q6N089 HUMAN | Q6N089 homo sapien |

Query Match 68.2% Score 442.5; DB 1; Length 119;

| | | | | | |
|----|-------|------|-----|----------------|---------------------|
| 32 | 416 | 64.1 | 116 | 2 Q9UL93 HUMAN | Q9UL93 homo sapien |
| 33 | 416 | 64.1 | 476 | 2 Q4V9Z4 MOUSE | Q4V9Z4 mus musculus |
| 34 | 415 | 63.9 | 616 | 2 Q504M7 MOUSE | Q504M7 mus musculus |
| 35 | 414 | 63.8 | 466 | 2 Q6N096 HUMAN | Q6N096 homo sapien |
| 36 | 413.5 | 63.7 | 122 | 1 HV3G HUMAN | P01768 homo sapien |
| 37 | 412.5 | 63.6 | 119 | 2 Q5F2I8 MOUSE | Q5F2I8 mus musculus |
| 38 | 412 | 63.5 | 146 | 2 Q924R8 MOUSE | Q924R8 mus musculus |
| 39 | 411.5 | 63.4 | 147 | 2 Q9Y509 HUMAN | Q9Y509 homo sapien |
| 40 | 410 | 63.2 | 466 | 2 Q6IN78 HUMAN | Q6IN78 homo sapien |
| 41 | 409.5 | 63.1 | 487 | 2 Q6ZVX0 HUMAN | Q6ZVX0 homo sapien |
| 42 | 409.5 | 63.1 | 573 | 2 Q8WU38 HUMAN | Q8WU38 homo sapien |
| 43 | 408.5 | 62.9 | 145 | 2 Q924B3 MOUSE | Q924B3 mus musculus |
| 44 | 408 | 62.9 | 117 | 1 HV42 MOUSE | P01812 mus musculus |
| 45 | 407.5 | 62.8 | 483 | 2 Q6MZX9 HUMAN | Q6MZX9 homo sapien |

ALIGNMENTS

RESULT 1

| ID | HV37 MOUSE | STANDARD; | PRT; | 119 AA. |
|----|--|-----------|------|---------|
| AC | P01807; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DB | Ig heavy chain V region X44. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; | | | |
| OC | Muroidea; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | PROTEIN SEQUENCE. | | | |
| RX | MEDLINE=79223895; PubMed=111245; | | | |
| RA | Rao D.N., Rudikoff S., Krutzsch H., Potter M.; | | | |
| RT | "Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions."; | | | |
| RT | determining regions."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979). | | | |
| RN | [2] | | | |
| RP | NUCLEOTIDE SEQUENCE OF 1-118. | | | |
| RX | MEDLINE=90064531; PubMed=2555519; | | | |
| RA | Miller A. III, Glasel J.A.; | | | |
| RT | "Comparative sequence and immunochemical analyses of murine monoclonal anti-morphine antibodies."; | | | |
| RT | J. Mol. Biol. 209:763-778 (1989). | | | |
| CC | -I- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein that binds galactan. | | | |
| CC | -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain. | | | |
| CC | This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. | | | |
| DR | PIR; A02077; AVMSX4. | | | |
| DR | HSPF; P01810; 2FBJ. | | | |
| DR | SMR; P01807; 1-119. | | | |
| DR | Ensembl; ENSMUSG00000003483; Mus musculus. | | | |
| DR | InterPro; IPR007110; Ig-like. | | | |
| DR | InterPro; IPR003596; Ig_v. | | | |
| DR | SMART; SM00406; IGV; 1. | | | |
| DR | PROSITE; PS00835; IG_LIKE; 1. | | | |
| KW | Direct protein sequencing; Immunoglobulin domain; | | | |
| KW | Immunoglobulin V region. | | | |
| FT | DOMAIN 1 117 Ig-like. | | | |
| FT | NON TER 119 119 | | | |
| SQ | SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64; | | | |

Best Local Similarity 67.8%; Pred. No. 3e-39;
Matches 82; Conservative 19; Mismatches 17; Indels 3; Gaps 2;

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QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFTGHWNWVRQAPGKGLVWGMITAPASSSTRY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVKLSEGGGLVQPGGSLRLSCKASGDFSFYSYMSWVRQAPGKGLVWGMITAPASSSTRY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDRFTTSVDKSKNTLYLQMSLRADTAAYVYCARGIYFYGTTFDYWGQGTLLTVTS 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TPSLKDRFTTSVDKSKNTLYLQMSLRADTAAYVYCAR-LHYIG--YAAVWGQGTLLTVTS 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 S 121
    :
Db 118 A 118
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RESULT 2

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Q6GMX2 HUMAN
ID Q6GMX2 HUMAN PRELIMINARY; PRT; 493 AA.
AC Q6GMX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHAI protein.
GN Name=IGHAI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073771; AAH73771.1; -; mRNA.
DR SMR; Q6GMX2; 263-471.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-Bet; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 493 AA; 52865 MW; 55B999305B286203 CRC64;
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Query Match 68.1%; Score 442; DB 2; Length 493;
Best Local Similarity 71.1%; Pred. No. 1.8e-38;
Matches 86; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFTGHWNWVRQAPGKGLVWGMITAPASSSTRY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVQPGGSLRLSCKASGDFSFYSYMSWVRQAPGKGLVWVRISNDSGSTSY 79
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDRFTTSVDKSKNTLYLQMSLRADTAAYVYCARGIYFYGTTFDYWGQGTLLTVTS 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADSVKGRTTSRDNAKNTLYLQMSLRGDAAYVYCARGFVSLPRSTLDINGQGTMTVTS 139
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 S 121
    :
Db 140 S 140
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RESULT 3

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Q96BB9 HUMAN
ID Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT chains of a human monoclonal antibody with broad reactivity to
RT malignant tumor cells."
RL Nucleic Acids Res. 17:4385-0 (1989).
DR EMBL; BC015760; AAH15760.1; -; mRNA.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSPP; P01861; 1ADQ.
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DR InterPro: IPR003596; IG v.
DR Pfam: PF07654; Cl-set; 2.
DR SMART: SM00409; IG; 3.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IGc1; 3.
DR PROSITE: PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1692EF3457BB686E CRC64;

Query Match 67.2%; Score 436; DB 2; Length 479;
Best Local Similarity 66.9%; Pred. No. 7.6e-38;
Matches 81; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMWVWVQAPGKGLWGMIAPIASSSTRY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVAGSGFSFNWMTWVIRQAPGKGLWVASITNTGGKTY 79
CY 61 NQKPKDFTISRDNAKSTLYLQMSLSRSEDATYYICTRAAHVWGPYYFAYWGQGVWTVS 120
EB 80 PDSVKGRTISRDNKSTLYLQMSLSRSEDATYYICTRAAHVWGPYYFAYWGQGVWTVS 139
CY 121 S 121
DB 140 S 140

RESULT 8
Q6PUA4 HUMAN
ID Q6PUA4 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PUA4
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
EN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Malek J.A., Gunaratne P.H.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RC NIH MGC Project;
RL EMBL: BC018747; AAH18747.1; -, mRNA.
DR HSSP: P01861; 1ADQ.
DR SMK: Q6PUA4; 20-470.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF07654; Cl-set; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 67.0%; Score 435; DB 2; Length 470;
Best Local Similarity 70.2%; Pred. No. 9.5e-38;
Matches 85; Conservative 9; Mismatches 27; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMWVWVQAPGKGLWGMIAPIASSSTRY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVVGFTFSYVMSWVQAPGKGLWVANIKQDGEKY 79
CY 61 NQKPKDFTISRDNAKSTLYLQMSLSRAEDTAVYICARGIYFYGTYYDYWGQGLTVTVS 120
DB 80 VDSVKGRTISRDNKSTLYLQMSLSRAEDTAVYICARDGSSWYRDWFDPMQGGTLTVTS 139
CY 121 S 121
DB 140 S 140

RESULT 9
Q569F4 HUMAN
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE IGHG1 protein.
EN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Malek J.A., Gunaratne P.H.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lymph;
RC NIH MGC Project;
RL EMBL: BC092518; AAH92518.1; -, mRNA.
DR EMBL: BC092518; AAH92518.1; -, mRNA.
```

| | | | | |
|-----------------------|-------|-------------------|------|----------------------------------|
| Query Match | 66.9% | Score 434.5 | DB 2 | Length 469 |
| Best Local Similarity | 73.0% | Pred. No. 1.1e-37 | | |
| Matches | 89 | Conservative | 9 | Mismatches 21; Indels 3; Gaps 2; |

| | | | |
|----|-----|-----------------------|---|
| QY | 1 | EVQLVESGGGLVQPGGSLRLS | CAASGYSTFGHWMVVRQAPGKLEWVGMIAPASSSTRY 60 |
| DB | 20 | EVQLVESGGGVVQPGGSLRLS | CAASGFTFDYAMHMYVRQAPGKLEWVSLISWDGGSTYY 79 |
| | | | : : |
| QY | 61 | NQPKDKRFTISVDSKNTLYLQ | NLSRAEDTAVYYCA-RGIYFYGTTFEDYWGQGLTVTV 119 |
| DB | 80 | ADSVKGRFTISRDNKNSLYLQ | NLSRAEDTALYYCATRG--GYSTAGFDYWGQGLTVTV 137 |
| | | | : : |
| QY | 120 | SS 121 | |
| | | | |
| DB | 138 | SS 139 | |


```

RESULT 10
Q6PI81 HUMAN
ID Q6PI81 HUMAN PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHM protein.
GN IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RX [1]
RX NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RX NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RX NIH NCG Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC041037; AAH41037.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; IGc1; 3.
DR SMART; SM00406; IG; 1.

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FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match 66.8%; Score 433.5; DB 1; Length 119;
Best Local Similarity 66.1%; Pred. No. 2.8e-38;
Matches 80; Conservative 20; Mismatches 18; Indels 3; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRAQPGKGLWGMIAPASSTRY 60
Dd 1 EVKLESGGGLVQPGGSLRLSCAASGYPDFSKYMSWVRAQPGKGLWGIETHPDSTINY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVYVCARGIYFTYFDYWGQGLTVTS 120
Dd 61 TPSLKDFRTISRDNAKNSLYLQMSKVRSEDTALYYCAR-LHYYG--YNAYWGQGLTVTS 117
QY 121 S 121
Dd 118 A 118

RESULT 12
Q9UL71_HUMAN
ID Q9UL71_HUMAN PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251 (1992).
DR EMBL; AF035042; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2PBA.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 66.1%; Score 429; DB 2; Length 113;
Best Local Similarity 70.2%; Pred. NO. 8e-38;
Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRAQPGKGLWGMIAPASSTRY 60
Dd 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRAQPGKGLWVAFIRYDGSNKTY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVYVCARGIYFTYFDYWGQGLTVTS 120
Dd 61 ADSVKGRTISRDNSKNTLYLQMSLRAEDTAVYVCARDL-----NYWGQGLTVTS 112
QY 121 S 121
Dd 113 S 113

Query Match 66.7%; Score 433; DB 2; Length 121;
Best Local Similarity 69.6%; Pred. No. 3.2e-38;
Matches 87; Conservative 11; Mismatches 19; Indels 8; Gaps 2;

```

```

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRAQPGKGLWGMIAPASSTRY 60
Dd 1 EVQLVESGGGVQPGGSLRLSCAASGFTFDYGMHWVRAQPGKGLWVSLSGDGGSTYY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVYVCARGIYFTYFDYWGQGLTVTS 116
Dd 61 ADSVKGRTISRDNSKNTLYLQMSLRAEDTALYYCAKGVKVTIY----DRPDIWGQGTM 116
QY 117 VTSS 121
Dd 117 VTSS 121

RESULT 13
Q9UL90_HUMAN
ID Q9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251 (1992).
DR EMBL; AF035042; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2PBA.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 66.1%; Score 429; DB 2; Length 113;
Best Local Similarity 70.2%; Pred. NO. 8e-38;
Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRAQPGKGLWGMIAPASSTRY 60
Dd 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRAQPGKGLWVAFIRYDGSNKTY 60

QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVYVCARGIYFTYFDYWGQGLTVTS 120
Dd 61 ADSVKGRTISRDNSKNTLYLQMSLRAEDTAVYVCARDL-----NYWGQGLTVTS 112
QY 121 S 121
Dd 113 S 113

```


| Result No. | Score | Query % | | Length | DB | ID | Description |
|------------|-------|---------|-----|--------|------------------|-------------------|-------------|
| | | Match | | | | | |
| 1 | 649 | 100.0 | 121 | 3 | US-09-725-798-24 | Sequence 24, Appl | |
| 2 | 649 | 100.0 | 121 | 4 | US-10-727-737-17 | Sequence 17, Appl | |
| 3 | 632 | 97.4 | 121 | 3 | US-09-795-798-5 | Sequence 5, Appl | |
| 4 | 632 | 97.4 | 121 | 4 | US-10-727-737-5 | Sequence 5, Appl | |
| 5 | 632 | 97.4 | 121 | 5 | US-10-877-532-6 | Sequence 6, Appl | |
| 6 | 632 | 97.4 | 451 | 4 | US-10-423-299-4 | Sequence 4, Appl | |
| 7 | 548.5 | 84.5 | 116 | 3 | US-09-726-258-50 | Sequence 50, Appl | |
| 8 | 520.5 | 80.2 | 122 | 5 | US-10-835-641-20 | Sequence 20, Appl | |
| 9 | 517.5 | 79.7 | 452 | 5 | US-10-861-049-46 | Sequence 46, Appl | |
| 10 | 517.5 | 79.7 | 452 | 6 | US-11-021-874-46 | Sequence 46, Appl | |
| 11 | 516.5 | 79.6 | 122 | 4 | US-10-818-765-2 | Sequence 2, Appl | |
| 12 | 516.5 | 79.6 | 122 | 5 | US-10-877-363-2 | Sequence 2, Appl | |
| 13 | 516.5 | 79.6 | 122 | 5 | US-10-822-651-2 | Sequence 2, Appl | |
| 14 | 516.5 | 79.6 | 122 | 5 | US-10-861-049-14 | Sequence 14, Appl | |
| 15 | 516.5 | 79.6 | 122 | 6 | US-11-021-874-14 | Sequence 14, Appl | |
| 16 | 516.5 | 79.6 | 122 | 6 | US-11-005-677-2 | Sequence 2, Appl | |
| 17 | 516.5 | 79.6 | 122 | 6 | US-11-006-136-2 | Sequence 2, Appl | |
| 18 | 516.5 | 79.6 | 452 | 4 | US-10-818-765-4 | Sequence 4, Appl | |
| 19 | 516.5 | 79.6 | 452 | 5 | US-10-861-049-16 | Sequence 16, Appl | |
| 20 | 516.5 | 79.6 | 452 | 5 | US-10-861-049-17 | Sequence 17, Appl | |
| 21 | 516.5 | 79.6 | 452 | 5 | US-10-861-049-20 | Sequence 20, Appl | |
| 22 | 516.5 | 79.6 | 452 | 5 | US-10-861-049-22 | Sequence 22, Appl | |
| 23 | 516.5 | 79.6 | 452 | 6 | US-11-021-874-16 | Sequence 16, Appl | |
| 24 | 516.5 | 79.6 | 452 | 6 | US-11-021-874-17 | Sequence 17, Appl | |
| 25 | 516.5 | 79.6 | 452 | 6 | US-11-021-874-20 | Sequence 20, Appl | |
| 26 | 516.5 | 79.6 | 452 | 6 | US-11-021-874-22 | Sequence 22, Appl | |
| 27 | 516.5 | 79.6 | 452 | 6 | US-11-005-677-4 | Sequence 4, Appl | |

Qy 61 NQKFKDRFTTISVDKSKNTLYLQMSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 Db 61 NQKFKDRFTTISVDKSKNTLYLQMSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120

Qy 121 \$ 121
 Db 121 \$ 121

RESULT 2

US-10-727-737-17
 ; Sequence 17, Application US/10727737
 ; Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
 ; Jardieu, Paula M.
 TITLE OF INVENTION: Antibody Mutants
 ;
 NUMBER OF SEQUENCES: 79
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ADDRESSEE: Genentech, Inc.
 ;
 STREET: 1 DNA Way
 ;
 CITY: South San Francisco
 ;
 STATE: California
 ;
 COUNTRY: USA
 ;
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ;
 COMPUTER: IBM PC compatible
 ;
 OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
 SOFTWARE: WinPatIn (Genentech)
 ;
 CURRENT APPLICATION DATA:
 ;
 APPLICATION NUMBER: US/10/727,737
 ;
 FILING DATE: 03-Dec-2003
 ;
 CLASSIFICATION: <Unknown>
 ;
 PRIOR APPLICATION DATA:
 ;
 APPLICATION NUMBER: US/08/975,329B
 ;
 FILING DATE: 20-Nov-1997
 ;
 APPLICATION NUMBER: 60/031945
 ;
 FILING DATE: 27-NOV-1996
 ;
 ATTORNEY/AGENT INFORMATION:
 ;
 NAME: Lee, Wendy M.
 ;
 REGISTRATION NUMBER: 40,378
 ;
 REFERENCE/DOCKET NUMBER: P1064R1
 ;
 TELECOMMUNICATION INFORMATION:
 ;
 TELEPHONE: 650/225-1994
 ;
 TELEFAX: 650/952-9881
 ;

INFORMATION FOR SEQ ID NO: 17:
 ;
 SEQUENCE CHARACTERISTICS:
 ;
 LENGTH: 121 amino acids
 ;
 TYPE: Amino Acid
 ;
 TOPOLOGY: Linear
 ;
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-10-727-737-17
 Query Match 100.0%; Score 649; DB 4; Length 121;
 Best Local Similarity 100.0%; Pred. No. 7.8e-52;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWVGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWVGMIAPASSSTRY 60

Qy 61 NQKFKDRFTTISVDKSKNTLYLQMSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 Db 61 NQKFKDRFTTISVDKSKNTLYLQMSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120

Qy 121 \$ 121
 Db 121 \$ 121

RESULT 3

US-09-795-798-5

; Sequence 5, Application US/09795798
 ; Publication No. US20030207336A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
 ; Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ;
 NUMBER OF SEQUENCES: 24
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ADDRESSEE: Genentech, Inc.
 ;
 STREET: 1 DNA Way
 ;
 CITY: South San Francisco
 ;
 STATE: California
 ;
 COUNTRY: USA
 ;
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ;
 COMPUTER: IBM PC compatible
 ;
 OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
 SOFTWARE: WinPatIn (Genentech)
 ;
 CURRENT APPLICATION DATA:
 ;
 APPLICATION NUMBER: US/09/795,798
 ;
 FILING DATE: 28-Feb-2001
 ;
 CLASSIFICATION: <Unknown>
 ;
 PRIOR APPLICATION DATA:
 ;
 APPLICATION NUMBER: 08/974,899
 ;
 FILING DATE: <Unknown>
 ;
 ATTORNEY/AGENT INFORMATION:
 ;
 NAME: Lee, Wendy M.
 ;
 REGISTRATION NUMBER: 40,378
 ;
 REFERENCE/DOCKET NUMBER: P1014R1
 ;
 TELECOMMUNICATION INFORMATION:
 ;
 TELEPHONE: 650/225-1994
 ;
 TELEFAX: 650/952-9881
 ;
 INFORMATION FOR SEQ ID NO: 5:
 ;
 SEQUENCE CHARACTERISTICS:
 ;
 LENGTH: 121 amino acids
 ;
 TYPE: Amino Acid
 ;
 TOPOLOGY: Linear
 ;
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-795-798-5
 Query Match 97.4%; Score 632; DB 3; Length 121;
 Best Local Similarity 96.7%; Pred. No. 2.8e-50;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWVGMIAPASSSTRY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLVWVGMIHPSDSETRY 60

Qy 61 NQKFKDRFTTISVDKSKNTLYLQMSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120
 Db 61 NQKFKDRFTTISVDKSKNTLYLQMSLRAEDTAVVYCARGIYFYGTTFDYWGQGLTVTS 120

Qy 121 \$ 121
 Db 121 \$ 121

RESULT 4

US-10-727-737-5
 ; Sequence 5, Application US/10727737
 ; Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
 ; Jardieu, Paula M.
 TITLE OF INVENTION: Antibody Mutants
 ;
 NUMBER OF SEQUENCES: 79
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ADDRESSEE: Genentech, Inc.
 ;
 STREET: 1 DNA Way
 ;
 CITY: South San Francisco
 ;
 STATE: California

```
;
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
US-10-727-737-5
Query Match 97.4%; Score 632; DB 4; Length 121;
Best Local Similarity 96.7%; Pred. No. 2.8e-50;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWGMIAPIASSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWGMIAPIASSTRY 60

Qy 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFGTYFDYWGQGLTVTVS 120
Db 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFGTYFDYWGQGLTVTVS 120

Qy 121 S 121
Db 121 S 121

RESULT 6
US-10-423-299-4
; Sequence 4, Application US/10423299
; Publication No. US20030229212A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT
; APPLICANT: FOLLMAN, DEBORAH
; APPLICANT: LEBRETON, BENEDICTE
; APPLICANT: VAN REIS, ROBERT
; TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
; FILE REFERENCE: 39766-0121A
; CURRENT APPLICATION NUMBER: US/10/423,299
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,953
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-423-299-4
Query Match 97.4%; Score 632; DB 4; Length 451;
Best Local Similarity 96.7%; Pred. No. 1.1e-49;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWGMIAPIASSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWGMIAPIASSTRY 60

Qy 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFGTYFDYWGQGLTVTVS 120
Db 61 NQKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFGTYFDYWGQGLTVTVS 120

Qy 121 S 121
Db 121 S 121

RESULT 7
US-09-726-258-50
; Sequence 50, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
;
US-10-877-532-6
; Sequence 6, Application US/10877532
; Publication No. US20050038231A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT L.
; APPLICANT: LAVERDIERE, AMY
; APPLICANT: MCDONALD, PAUL J.
; APPLICANT: O'LEARY, RHONA M.
; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
; FILE REFERENCE: P2015R1
; CURRENT APPLICATION NUMBER: US/10/877,532
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,500
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 6
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-6
Query Match 97.4%; Score 632; DB 5; Length 121;
```

```
; STREET: 1 DNA Way
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; US-09-726-258-50

Query Match 84.5%; Score 548.5; DB 3; Length 116;
Best Local Similarity 88.8%; Pred. No. 1.2e-42;
Matches 103; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNVRRQAPGKGLVWGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNVRRQAPGKGLVWGMIHPDSETRY 60

Qy 61 NQKFKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYC-ARGIFYFGTTFYFDYWGQGT 115
Db 61 ADSVKGRFTTISRDNSKNTLYLQMNLSRAEDTAVYYCAARGIFYFGTTFYFDYWGQGT 116

RESULT 8
US-10-835-641-20
; Sequence 20, Application US/10835641
; Publication No. US20040236078A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESTRA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/835,641
; FILING DATE: 30-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-Nov-2000
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-835-641-20

Query Match 80.2%; Score 520.5; DB 5; Length 122;
Best Local Similarity 83.7%; Pred. No. 4.8e-40;
Matches 103; Conservative 4; Mismatches 13; Indels 3; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNVRRQAPGKGLVWGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNVRRQAPGKGLVWALINPYKGVSTY 60

Qy 61 NQKFKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARGIFYFGTTFYFDYWGQGT 118
Db 61 NQKFKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARGSY-YGDSWDYFDVWGQGT 119

Qy 119 VSS 121
Db 120 VSS 122

RESULT 9
US-10-861-049-46
; Sequence 46, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 46
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-861-049-46

Query Match 79.7%; Score 517.5; DB 5; Length 452;
Best Local Similarity 82.0%; Pred. No. 3.4e-39;
Matches 100; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMNNVRRQAPGKGLVWGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNNHVVRRQAPGKGLVWGIYPGNGATSY 60
```

QY 61 NQKPKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGT-TYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARVWVYSASYWYFDVWGQGLTVTV 120

QY 120 SS 121
Db 121 SS 122

RESULT 10

US-11-021-874-46
; Sequence 46, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 46
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-021-874-46

Query Match 79.7%; Score 517.5; DB 6; Length 452;
Best Local Similarity 82.0%; Pred. No. 3.4e-39;
Matches 100; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWVGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWVGMIAPASSSTRY 60

QY 61 NQKPKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGT-TYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARVWVYSASYWYFDVWGQGLTVTV 120

QY 120 SS 121
Db 121 SS 122

RESULT 11

US-10-818-765-2
; Sequence 2, Application US/10818765
; Publication No. US20040202658A1
; GENERAL INFORMATION:
; APPLICANT: Benyunes, Mark C.
; TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
; TITLE OF INVENTION: INADEQUATE RESPONSE TO A TNF-a INHIBITOR
; FILE REFERENCE: P2027R1-US
; CURRENT APPLICATION NUMBER: US/10/818,765
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: US 60/461,4819
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence

; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-818-765-2

Query Match 79.6%; Score 516.5; DB 4; Length 122;
Best Local Similarity 82.0%; Pred. No. 1.1e-39;
Matches 100; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWVGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWVGMIAPASSSTRY 60

QY 61 NQKPKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGT-TYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARVWVYSASYWYFDVWGQGLTVTV 120

QY 120 SS 121
Db 121 SS 122

RESULT 12

US-10-877-363-2
; Sequence 2, Application US/10877363
; Publication No. US20050032130A1
; GENERAL INFORMATION:
; APPLICANT: BERESINI, MAUREEN
; APPLICANT: SONG, AN
; TITLE OF INVENTION: NEUTRALIZING ANTIBODY ASSAY AND USES THEREFOR
; FILE REFERENCE: P2032R1
; CURRENT APPLICATION NUMBER: US/10/877,363
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,678
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-877-363-2

Query Match 79.6%; Score 516.5; DB 5; Length 122;
Best Local Similarity 82.0%; Pred. No. 1.1e-39;
Matches 100; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWVGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWVGMIAPASSSTRY 60

QY 61 NQKPKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIYFYGT-TYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTISVDKSKNTLYLQMNLSRAEDTAVVYCARVWVYSASYWYFDVWGQGLTVTV 120

QY 120 SS 121
Db 121 SS 122

RESULT 13

US-10-922-651-2
; Sequence 2, Application US/10922651
; Publication No. US20050053602A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; TITLE OF INVENTION: Therapy of Ocular Disorders
; FILE REFERENCE: P2029R1
; CURRENT APPLICATION NUMBER: US/10/922,651
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/498,791
; PRIOR FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 4

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; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-922-651-2

Query Match          79.6%; Score 516.5; DB 5; Length 122;
Best Local Similarity 82.0%; Pred. No. 1.1e-39;
Matches 100; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTGHWNWVRQAPGKLEWVGMIAPASSSTRY 60
    |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTTSYNNHWVRQAPGKLEWVGAIYPGNGDTSY 60
    |||||

Qy 61 NQKFKDRTTISVDKSKNTLYLQNNSLRAEDTAVYVCARGIFYGT-TYFDYWGQGLTVTV 119
    |||||
Db 61 NQKFKGRFTTISVDKSKNTLYLQNNSLRAEDTAVYVCARVVYSNSYWFYFDYWGQGLTVTV 120
    |||||

Qy 120 SS 121
    ||
Db 121 SS 122
```

```
RESULT 14
US-10-861-049-14
; Sequence 14, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861.049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-861-049-14
```

```
Query Match          79.6%; Score 516.5; DB 5; Length 122;
Best Local Similarity 82.0%; Pred. No. 1.1e-39;
Matches 100; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTGHWNWVRQAPGKLEWVGMIAPASSSTRY 60
    |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTTSYNNHWVRQAPGKLEWVGAIYPGNGDTSY 60
    |||||

Qy 61 NQKFKDRTTISVDKSKNTLYLQNNSLRAEDTAVYVCARGIFYGT-TYFDYWGQGLTVTV 119
    |||||
Db 61 NQKFKGRFTTISVDKSKNTLYLQNNSLRAEDTAVYVCARVVYSNSYWFYFDYWGQGLTVTV 120
    |||||

Qy 120 SS 121
    ||
Db 121 SS 122
```

```
RESULT 15
US-11-021-874-14
; Sequence 14, Application US/11021874
; Publication No. US20050163775A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021.874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 14
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-021-874-14
```

```
Query Match          79.6%; Score 516.5; DB 6; Length 122;
Best Local Similarity 82.0%; Pred. No. 1.1e-39;
Matches 100; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTGHWNWVRQAPGKLEWVGMIAPASSSTRY 60
    |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTTSYNNHWVRQAPGKLEWVGAIYPGNGDTSY 60
    |||||

Qy 61 NQKFKDRTTISVDKSKNTLYLQNNSLRAEDTAVYVCARGIFYGT-TYFDYWGQGLTVTV 119
    |||||
Db 61 NQKFKGRFTTISVDKSKNTLYLQNNSLRAEDTAVYVCARVVYSNSYWFYFDYWGQGLTVTV 120
    |||||

Qy 120 SS 121
    ||
Db 121 SS 122
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Search completed: April 13, 2006, 17:24:37
Job time : 119.886 secs

GenCore version 5.1.7
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CM protein - protein search, using sw model

Run on: April 13, 2006, 17:21:05 ; Search time 17.9651 Seconds
(without alignments)
286.178 Million cell updates/sec

Title: US-10-727-737-17

Perfect score: 649

Sequence: 1 EVQLVSGGHLVQPGSLRL.....PYGTTYDYWGQGLTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /SID85/prodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SID85/prodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SID85/prodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SID85/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SID85/prodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SID85/prodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SID85/prodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SID85/prodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 649 | 100.0 | 121 | 6 | US-10-665-658-24 |
| 2 | 632 | 97.4 | 121 | 6 | US-10-665-658-5 |
| 3 | 632 | 97.4 | 121 | 7 | US-11-107-028-50 |
| 4 | 632 | 97.4 | 121 | 7 | US-11-149-031-2 |
| 5 | 632 | 97.4 | 121 | 7 | US-11-208-422-14 |
| 6 | 521.5 | 80.4 | 122 | 7 | US-11-120-338-24 |
| 7 | 521.5 | 80.4 | 122 | 7 | US-11-143-077-24 |
| 8 | 521.5 | 80.4 | 122 | 7 | US-11-143-386-24 |
| 9 | 521.5 | 80.4 | 122 | 7 | US-11-187-364-36 |
| 10 | 521.5 | 80.4 | 122 | 7 | US-11-208-422-45 |
| 11 | 521.5 | 80.4 | 451 | 7 | US-11-120-338-25 |
| 12 | 521.5 | 80.4 | 451 | 7 | US-11-143-077-22 |
| 13 | 521.5 | 80.4 | 451 | 7 | US-11-143-386-25 |
| 14 | 521.5 | 80.4 | 451 | 7 | US-11-187-364-34 |
| 15 | 521.5 | 80.4 | 452 | 7 | US-11-120-338-17 |
| 16 | 521.5 | 80.4 | 452 | 7 | US-11-107-028-47 |
| 17 | 521.5 | 80.4 | 452 | 7 | US-11-106-820-45 |
| 18 | 521.5 | 80.4 | 452 | 7 | US-11-143-077-17 |
| 19 | 521.5 | 80.4 | 452 | 7 | US-11-143-386-17 |
| 20 | 521.5 | 80.4 | 452 | 7 | US-11-208-422-46 |
| 21 | 517.5 | 79.7 | 122 | 7 | US-11-208-422-42 |
| 22 | 517.5 | 79.7 | 452 | 7 | US-11-107-028-43 |
| 23 | 517.5 | 79.7 | 452 | 7 | US-11-107-028-45 |
| 24 | 517.5 | 79.7 | 452 | 7 | US-11-107-028-46 |
| 25 | 517.5 | 79.7 | 452 | 7 | US-11-106-820-30 |

| | | | | | | |
|----|-------|------|-----|---|------------------|-------------------|
| 26 | 517.5 | 79.7 | 452 | 7 | US-11-208-422-40 | Sequence 40, Appl |
| 27 | 517.5 | 79.7 | 452 | 7 | US-11-208-422-43 | Sequence 43, Appl |
| 28 | 517.5 | 79.7 | 452 | 7 | US-11-208-422-44 | Sequence 44, Appl |
| 29 | 516.5 | 79.6 | 122 | 7 | US-11-120-338-8 | Sequence 8, Appl |
| 30 | 516.5 | 79.6 | 122 | 7 | US-11-107-028-30 | Sequence 30, Appl |
| 31 | 516.5 | 79.6 | 122 | 7 | US-11-106-820-8 | Sequence 8, Appl |
| 32 | 516.5 | 79.6 | 122 | 7 | US-11-143-077-8 | Sequence 8, Appl |
| 33 | 516.5 | 79.6 | 122 | 7 | US-11-190-364-8 | Sequence 8, Appl |
| 34 | 516.5 | 79.6 | 122 | 7 | US-11-147-780-8 | Sequence 8, Appl |
| 35 | 516.5 | 79.6 | 122 | 7 | US-11-143-386-8 | Sequence 8, Appl |
| 36 | 516.5 | 79.6 | 122 | 7 | US-11-187-364-8 | Sequence 8, Appl |
| 37 | 516.5 | 79.6 | 122 | 7 | US-11-208-422-2 | Sequence 2, Appl |
| 38 | 516.5 | 79.6 | 451 | 7 | US-11-120-338-22 | Sequence 22, Appl |
| 39 | 516.5 | 79.6 | 451 | 7 | US-11-143-386-22 | Sequence 22, Appl |
| 40 | 516.5 | 79.6 | 452 | 7 | US-11-120-338-14 | Sequence 14, Appl |
| 41 | 516.5 | 79.6 | 452 | 7 | US-11-120-338-15 | Sequence 15, Appl |
| 42 | 516.5 | 79.6 | 452 | 7 | US-11-107-028-32 | Sequence 32, Appl |
| 43 | 516.5 | 79.6 | 452 | 7 | US-11-107-028-33 | Sequence 33, Appl |
| 44 | 516.5 | 79.6 | 452 | 7 | US-11-106-820-26 | Sequence 26, Appl |
| 45 | 516.5 | 79.6 | 452 | 7 | US-11-106-820-28 | Sequence 28, Appl |

ALIGNMENTS

RESULT 1
US-10-665-658-24
; Sequence 24, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/POCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24

Query Match 100.0%; Score 649; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 3e-46;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60

QY 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIFYGTTTFDYWGQGLTLVTVS 120
 DB 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIFYGTTTFDYWGQGLTLVTVS 120

QY 121 S 121
 DB 121 S 121

RESULT 2
 US-10-665-658-5
 ; Sequence 5, Application US/10665658
 ; Publication No. US20050276801A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/665,658
 ; FILING DATE: 19-Sep-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/031971
 ; FILING DATE: 27-NOV-1996
 ; APPLICATION NUMBER: 08/974899
 ; FILING DATE: 20-NOV-1997
 ; APPLICATION NUMBER: 09/420745
 ; FILING DATE: 20-OCT-1999
 ; APPLICATION NUMBER: 09/975798
 ; FILING DATE: 28-FEB-2001
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tan, Lee K.
 ; REGISTRATION NUMBER: 39,447
 ; REFERENCE/DOCKET NUMBER: P1014R1CID1C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-4462
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 121 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-665-658-5

Query Match 97.4%; Score 632; DB 6; Length 121;
 Best Local Similarity 96.7%; Pred. No. 7.3e-45;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60

DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
 QY 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIFYGTTTFDYWGQGLTLVTVS 120
 DB 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIFYGTTTFDYWGQGLTLVTVS 120

QY 121 S 121
 DB 121 S 121

RESULT 3
 US-11-107-028-50
 ; Sequence 50, Application US/11107028
 ; Publication No. US20050276803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHAN, ANDREW C.
 ; APPLICANT: GONG, QIAN
 ; APPLICANT: MARTIN, FLAVIUS
 ; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
 ; FILE REFERENCE: P2112R1
 ; CURRENT APPLICATION NUMBER: US/11/107,028
 ; PRIOR FILING DATE: 2005-04-15
 ; PRIOR APPLICATION NUMBER: US 60/563,263
 ; PRIOR FILING DATE: 2004-04-16
 ; NUMBER OF SEQ ID NOS: 52
 ; SEQ ID NO 50
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence is synthesized

US-11-107-028-50

Query Match 97.4%; Score 632; DB 7; Length 121;
 Best Local Similarity 96.7%; Pred. No. 7.3e-45;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTFGHMNNVVRQAPGKLEWVGMIAPASSSTRY 60

QY 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIFYGTTTFDYWGQGLTLVTVS 120
 DB 61 NQPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVVYCARGIFYGTTTFDYWGQGLTLVTVS 120

QY 121 S 121
 DB 121 S 121

RESULT 4
 US-11-149-031-2
 ; Sequence 2, Application US/11149031
 ; Publication No. US20060013818A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COFFE, BERNARD S.
 ; TITLE OF INVENTION: Method of Treating Granuloma Annulare or Sarcoid
 ; FILE REFERENCE: P2129R1
 ; CURRENT APPLICATION NUMBER: US/11/149,031
 ; CURRENT FILING DATE: 2005-06-08
 ; PRIOR APPLICATION NUMBER: US 60/578,768
 ; PRIOR FILING DATE: 2004-06-09
 ; PRIOR APPLICATION NUMBER: US 60/579,096
 ; PRIOR FILING DATE: 2004-06-10
 ; NUMBER OF SEQ ID NOS: 4
 ; SEQ ID NO 2
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence is synthesized

US-11-149-031-2

; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-24

Query Match 80.4%; Score 521.5; DB 7; Length 122;
Best Local Similarity 82.8%; Pred. No. 6.8e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWGMIAPIASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTSYNNHWWVRQAPGKGLWGMIAPIPGNGATSY 60

Qy 61 NQKPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARGIYF-YGTTYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARVVIYSYRYWYFDYWGQGLTVTV 120

Qy 120 SS 121
Db 121 SS 122

RESULT 9
US-11-187-364-36
; Sequence 36, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitraya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 36
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-36

Query Match 80.4%; Score 521.5; DB 7; Length 122;
Best Local Similarity 82.8%; Pred. No. 6.8e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWGMIAPIASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTSYNNHWWVRQAPGKGLWGMIAPIPGNGATSY 60

Qy 61 NQKPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARGIYF-YGTTYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARVVIYSYRYWYFDYWGQGLTVTV 120

Qy 120 SS 121
Db 121 SS 122

RESULT 10
US-11-208-422-45
; Sequence 45, Application US/11208422

; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 45
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-45

Query Match 80.4%; Score 521.5; DB 7; Length 122;
Best Local Similarity 82.8%; Pred. No. 6.8e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWGMIAPIASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTSYNNHWWVRQAPGKGLWGMIAPIPGNGATSY 60

Qy 61 NQKPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARGIYF-YGTTYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARVVIYSYRYWYFDYWGQGLTVTV 120

Qy 120 SS 121
Db 121 SS 122

RESULT 11
US-11-120-338-25
; Sequence 25, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-25

Query Match 80.4%; Score 521.5; DB 7; Length 451;
Best Local Similarity 82.8%; Pred. No. 2e-35;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLWGMIAPIASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTSYNNHWWVRQAPGKGLWGMIAPIPGNGATSY 60

Qy 61 NQKPKDRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARGIYF-YGTTYFDYWGQGLTVTV 119
Db 61 NQKPKGRFTTISVDKSKNTLYLQMNLSRAEDTAVYYCARVVIYSYRYWYFDYWGQGLTVTV 120

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1 EVQLVESGGGLVQPGGSLRLSQAASGYFTTSYNMHWVRQAPKGLEWVGAIYPGNGATSY 60
61 NQKPKDRFTISVDKSKNTLYLQMSLRAEDTAVYYCARGIYF-YGTTTFDYWGQGLTLTV 119
61 NQKPKGRFTISVDKSKNTLYLQMSLRAEDTAVYYCARVYYSRYWTFDYWGQGLTLTV 120
120 SS 121
121 SS 122
121 SS 122

RESULT 14
US-11-187-364-34
; Sequence 34, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitraya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P214981
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 34
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-34

Query Match 80.4%; Score 521.5; DB 7; Length 451;
Best Local Similarity 82.8%; Pred. No. 2e-35;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSQAASGYFTTSYNMHWVRQAPKGLEWVGAIYPGNGATSY 60
DB 1 EVQLVESGGGLVQPGGSLRLSQAASGYFTTSYNMHWVRQAPKGLEWVGAIYPGNGATSY 60
QY 61 NQKPKDRFTISVDKSKNTLYLQMSLRAEDTAVYYCARGIYF-YGTTTFDYWGQGLTLTV 119
DB 61 NQKPKGRFTISVDKSKNTLYLQMSLRAEDTAVYYCARVYYSRYWTFDYWGQGLTLTV 120
120 SS 121
121 SS 122
121 SS 122

RESULT 15
US-11-120-338-17
; Sequence 17, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P207982
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 17
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-17

Query Match 80.4%; Score 521.5; DB 7; Length 452;
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Best Local Similarity 82.8%; Pred. NO. 2e-35;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTGHMMNVRQAPKGLEWVGMIAPASSSTRY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSTGHMMNVRQAPKGLEWVGMIAPASSSTRY 60
Qy 61 NQKPKDREFTISVDKSKNTLYLQMSLRABDTAVYYCARGIYP-YGTTVFYDVGQGLTVTV 119
Db 61 NQKPKGREFTISVDKSKNTLYLQMSLRABDTAVYYCARVYYSRYWYFDVWGQGLTVTV 120
Qy 120 SS 121
Db 121 SS 122

Search completed: April 13, 2006, 17:25:17
Job time : 17.9651 secs

GenCore version 5.1.7
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CM protein - protein search, using sw model

Run on: April 13, 2006, 17:21:05 ; Search time 16.0349 Seconds
(without alignments)
286.178 Million cell updates/sec

Title: US-10-727-737-2
Perfect score: 560
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTFGQGTKEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|------------------|
| 1 | 560 | 100.0 | 108 | 6 | US-10-665-658-2 |
| 2 | 560 | 100.0 | 108 | 7 | US-11-208-422-13 |
| 3 | 560 | 100.0 | 214 | 7 | US-11-208-422-15 |
| 4 | 555 | 99.1 | 107 | 7 | US-11-107-028-49 |
| 5 | 555 | 99.1 | 107 | 7 | US-11-149-031-1 |
| 6 | 506 | 90.4 | 108 | 6 | US-10-665-658-3 |
| 7 | 506 | 90.4 | 108 | 7 | US-11-120-338-3 |
| 8 | 506 | 90.4 | 108 | 7 | US-11-143-077-3 |
| 9 | 506 | 90.4 | 108 | 7 | US-11-190-364-3 |
| 10 | 506 | 90.4 | 108 | 7 | US-11-147-780-3 |
| 11 | 506 | 90.4 | 108 | 7 | US-11-143-386-3 |
| 12 | 506 | 90.4 | 108 | 7 | US-11-187-364-3 |
| 13 | 506 | 90.4 | 109 | 6 | US-10-981-356A-5 |
| 14 | 506 | 90.4 | 109 | 7 | US-11-096-046-5 |
| 15 | 501 | 89.5 | 107 | 7 | US-11-154-337-5 |
| 16 | 501 | 89.5 | 107 | 7 | US-11-182-908-5 |
| 17 | 501 | 89.5 | 107 | 7 | US-11-102-120-5 |
| 18 | 501 | 89.5 | 107 | 7 | US-11-223-361-5 |
| 19 | 501 | 89.5 | 107 | 7 | US-11-222-587-5 |
| 20 | 501 | 89.5 | 108 | 7 | US-11-106-820-3 |
| 21 | 501 | 89.5 | 109 | 6 | US-10-834-397-28 |
| 22 | 501 | 89.5 | 109 | 6 | US-10-834-397-43 |
| 23 | 497 | 88.8 | 108 | 6 | US-10-771-257-75 |
| 24 | 497 | 88.8 | 108 | 7 | US-11-127-677-75 |
| 25 | 496 | 88.6 | 107 | 7 | US-11-051-453-32 |

| | | | | | | |
|----|-----|------|-----|---|-------------------|-------------------|
| 26 | 496 | 88.6 | 129 | 7 | US-11-051-453-46 | Sequence 46, Appl |
| 27 | 495 | 88.4 | 109 | 7 | US-11-127-932-14 | Sequence 14, Appl |
| 28 | 495 | 88.4 | 109 | 7 | US-11-127-932-18 | Sequence 18, Appl |
| 29 | 495 | 88.4 | 109 | 7 | US-11-127-903-14 | Sequence 14, Appl |
| 30 | 495 | 88.4 | 109 | 7 | US-11-127-903-18 | Sequence 18, Appl |
| 31 | 493 | 88.0 | 108 | 6 | US-10-834-397-14 | Sequence 14, Appl |
| 32 | 492 | 87.9 | 214 | 7 | US-11-049-536-700 | Sequence 700, App |
| 33 | 492 | 87.9 | 214 | 7 | US-11-199-739-700 | Sequence 700, App |
| 34 | 492 | 87.9 | 214 | 7 | US-11-199-739-724 | Sequence 724, App |
| 35 | 491 | 87.7 | 234 | 7 | US-11-041-095-25 | Sequence 25, Appl |
| 36 | 491 | 87.7 | 239 | 7 | US-11-041-095-19 | Sequence 19, Appl |
| 37 | 491 | 87.7 | 290 | 7 | US-11-041-095-13 | Sequence 13, Appl |
| 38 | 490 | 87.5 | 107 | 7 | US-11-051-453-30 | Sequence 30, Appl |
| 39 | 490 | 87.5 | 108 | 6 | US-10-925-366A-3 | Sequence 3, Appl |
| 40 | 490 | 87.5 | 108 | 6 | US-10-925-366A-6 | Sequence 6, Appl |
| 41 | 490 | 87.5 | 108 | 7 | US-11-102-512-3 | Sequence 3, Appl |
| 42 | 490 | 87.5 | 108 | 7 | US-11-102-512-6 | Sequence 6, Appl |
| 43 | 490 | 87.5 | 108 | 7 | US-11-098-758-3 | Sequence 3, Appl |
| 44 | 490 | 87.5 | 108 | 7 | US-11-098-758-6 | Sequence 6, Appl |
| 45 | 490 | 87.5 | 111 | 7 | US-11-049-536-100 | Sequence 100, App |

ALIGNMENTS

RESULT 1
US-10-665-658-2
; Sequence 2, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Gardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-658-2

```
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-15

Query Match      100.0%; Score 560; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Qy 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIKR 108
Db 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIKR 108

RESULT 2
US-11-208-422-13
; Sequence 13, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2159R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 13
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-13

Query Match      100.0%; Score 560; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Qy 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIKR 108
Db 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIKR 108

RESULT 3
US-11-208-422-15
; Sequence 15, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2159R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 15
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-15

Query Match      100.0%; Score 560; DB 7; Length 214;
Best Local Similarity 100.0%; Pred. No. 5.9e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Qy 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIKR 108
Db 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIKR 108

RESULT 4
US-11-107-028-49
; Sequence 49, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 49
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-49

Query Match      99.1%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
Qy 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTITISSLPQEDPATYCCQHNEYPLTFGGQTKVEIK 107

RESULT 5
US-11-149-031-1
; Sequence 1, Application US/11149031
; Publication No. US20060013818A1
; GENERAL INFORMATION:
; APPLICANT: GOFFE, BERNARD S.
; TITLE OF INVENTION: Method of Treating Granuloma Annulare or Sarcoid
; FILE REFERENCE: P2129R1
; CURRENT APPLICATION NUMBER: US/11/149,031
; CURRENT FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: US 60/578,768
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/579,096
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
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; OTHER INFORMATION: sequence is synthesized
US-11-149-031-1

Query Match          99.1%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIK 107
Db 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIK 107

RESULT 6
US-10-665-658-3
; Sequence 3, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; PRESTA, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1CID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-665-658-3

Query Match          90.4%; Score 506; DB 6; Length 108;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYAASSLSGVS 60

Qy 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIK 108
Db 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIK 108
```

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Qy 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIKR 108
Db 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNSLPFTWTFGQGTKEIKR 108

RESULT 7
US-11-120-338-3
; Sequence 3, Application US/11120338
; Publication No. US20050271659A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-3

Query Match          90.4%; Score 506; DB 7; Length 108;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYAASSLSGVS 60

Qy 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIKR 108
Db 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNSLPFTWTFGQGTKEIKR 108

RESULT 8
US-11-143-077-3
; Sequence 3, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-3

Query Match          90.4%; Score 506; DB 7; Length 108;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRAKTIISKYLAWYQKPGKAPKLLIYAASSLSGVS 60

Qy 61 RFGSGSGTDFLTITSSLPQDPATYYCOQHNEYPVLTFGQGTKEIKR 108
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Db 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108
|||||

RESULT 9

US-11-190-364-3

; Sequence 3, Application US/11190364

; Publication No. US20060024300A1

; GENERAL INFORMATION:

; APPLICANT: Adams ET AL.

; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof

; FILE REFERENCE: P1990R3C1P1

; CURRENT APPLICATION NUMBER: US/11/190,364

; CURRENT FILING DATE: 2005-07-26

; PRIOR APPLICATION NUMBER: US 60/434,115

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: US 60/526,163

; PRIOR FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: PCT/US03/40426

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 11/147,780

; PRIOR FILING DATE: 2005-06-07

; NUMBER OF SEQ ID NOS: 38

; SEQ ID NO 3

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized

US-11-190-364-3

Query Match 90.4%; Score 506; DB 7; Length 108;

Best Local Similarity 89.8%; Pred. No. 7.9e-35;

Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Db 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Qy 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

Db 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

RESULT 10

US-11-147-780-3

; Sequence 3, Application US/11147780

; Publication No. US20060034835A1

; GENERAL INFORMATION:

; APPLICANT: Adams ET AL.

; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof

; FILE REFERENCE: P1990R3C1

; CURRENT APPLICATION NUMBER: US/11/147,780

; CURRENT FILING DATE: 2005-06-07

; PRIOR APPLICATION NUMBER: US 60/434,115

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: US 60/526,163

; PRIOR FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: PCT/US03/40426

; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 38

; SEQ ID NO 3

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized

US-11-147-780-3

Query Match 90.4%; Score 506; DB 7; Length 108;

Best Local Similarity 89.8%; Pred. No. 7.9e-35;

Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Db 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Qy 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

Db 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

Qy 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Db 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Qy 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

Db 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

RESULT 11

US-11-143-386-3

; Sequence 3, Application US/11143386

; Publication No. US20060051345A1

; GENERAL INFORMATION:

; APPLICANT: FROHNA, PAUL A.

; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS

; FILE REFERENCE: P2134R1

; CURRENT APPLICATION NUMBER: US/11/143,386

; CURRENT FILING DATE: 2005-06-02

; PRIOR APPLICATION NUMBER: US 60/576,993

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 25

; SEQ ID NO 3

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized.

US-11-143-386-3

Query Match 90.4%; Score 506; DB 7; Length 108;

Best Local Similarity 89.8%; Pred. No. 7.9e-35;

Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Db 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Qy 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

Db 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

RESULT 12

US-11-187-364-3

; Sequence 3, Application US/11187364

; Publication No. US20060062787A1

; GENERAL INFORMATION:

; APPLICANT: Hitraya, Elena

; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME

; FILE REFERENCE: P2149R1

; CURRENT APPLICATION NUMBER: US/11/187,364

; CURRENT FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US 60/590,302

; PRIOR FILING DATE: 2004-07-22

; NUMBER OF SEQ ID NOS: 36

; SEQ ID NO 3

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-187-364-3

Query Match 90.4%; Score 506; DB 7; Length 108;

Best Local Similarity 89.8%; Pred. No. 7.9e-35;

Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Db 1 DIQWTSPPSSLSASVGRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

|||||

Qy 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||

Db 61 RFGSGSGTDTLTITISSLPQDFATYCCQYNSLPWTFGGTKVEIKR 108

|||||


```
RESULT 13
US-10-981-356A-5
; Sequence 5, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P206981
; CURRENT APPLICATION NUMBER: US/10/981.356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-5

Query Match      90.4%; Score 506; DB 6; Length 109;
Best Local Similarity 89.8%; Pred. No. 8e-35;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTIISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISINYLAWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 108
Db 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 108

RESULT 14
US-11-096-046-5
; Sequence 5, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096.046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-5

Query Match      90.4%; Score 506; DB 7; Length 109;
Best Local Similarity 89.8%; Pred. No. 8e-35;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTIISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISINYLAWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 108
Db 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 108
```

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Db 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 108

RESULT 15
US-11-154-337-5
; Sequence 5, Application US/11154337
; Publication No. US20060013819A1
; GENERAL INFORMATION:
; APPLICANT: KELSEY, STEPHEN M.
; TITLE OF INVENTION: THERAPY OF PLATINUM-RESISTANT CANCER
; FILE REFERENCE: P2146R1
; CURRENT APPLICATION NUMBER: US/11/154.337
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/580,333
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-154-337-5

Query Match      89.5%; Score 501; DB 7; Length 107;
Best Local Similarity 89.7%; Pred. No. 2e-34;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTIISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISINYLAWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 107
Db 61 RFGSGSGTDTLTITISSLPQDPFATYYCQQNSLPWTFTGGTKVEIKR 107

Search completed: April 13, 2006, 17:25:18
Job time : 17.0349 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 17:19:49 ; Search time 106.114 Seconds
(without alignments)
425.257 Million cell updates/sec

Title: US-10-727-737-2
Perfect score: 560
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTFGQGTKEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 560 | 100.0 | 108 | 3 | US-09-795-798-2 |
| 2 | 560 | 100.0 | 108 | 4 | US-10-727-737-2 |
| 3 | 560 | 100.0 | 108 | 5 | US-10-877-532-5 |
| 4 | 560 | 100.0 | 214 | 4 | US-10-423-299-3 |
| 5 | 546.5 | 97.6 | 109 | 3 | US-09-726-258-47 |
| 6 | 506 | 90.4 | 108 | 3 | US-09-056-160B-12 |
| 7 | 506 | 90.4 | 108 | 3 | US-09-795-798-3 |
| 8 | 506 | 90.4 | 108 | 4 | US-10-234-671-12 |
| 9 | 506 | 90.4 | 108 | 4 | US-10-727-737-3 |
| 10 | 506 | 90.4 | 108 | 5 | US-10-861-049-38 |
| 11 | 506 | 90.4 | 108 | 5 | US-10-974-591-12 |
| 12 | 506 | 90.4 | 108 | 6 | US-11-021-874-38 |
| 13 | 506 | 90.4 | 109 | 3 | US-09-811-123-6 |
| 14 | 506 | 90.4 | 110 | 4 | US-10-044-896-4 |
| 15 | 505 | 90.2 | 127 | 3 | US-09-809-739-10 |
| 16 | 505 | 90.2 | 127 | 5 | US-10-662-061-10 |
| 17 | 505 | 90.2 | 233 | 4 | US-10-404-724-68 |
| 18 | 504 | 90.0 | 109 | 5 | US-10-835-641-3 |
| 19 | 502 | 89.6 | 108 | 5 | US-10-783-311-126 |
| 20 | 501 | 89.5 | 107 | 4 | US-10-268-501-5 |
| 21 | 501 | 89.5 | 107 | 4 | US-10-608-626-5 |
| 22 | 501 | 89.5 | 107 | 4 | US-10-600-152-14 |
| 23 | 501 | 89.5 | 107 | 4 | US-10-619-754-5 |
| 24 | 501 | 89.5 | 107 | 5 | US-10-835-641-18 |
| 25 | 501 | 89.5 | 107 | 5 | US-10-719-310-5 |
| 26 | 501 | 89.5 | 107 | 6 | US-11-044-749-5 |
| 27 | 501 | 89.5 | 107 | 6 | US-11-154-465-5 |

| | | | | | | |
|----|-----|------|-----|---|-------------------|-------------------|
| 28 | 501 | 89.5 | 108 | 4 | US-10-125-687-8 | Sequence 8, Appli |
| 29 | 501 | 89.5 | 108 | 5 | US-10-996-191-8 | Sequence 8, Appli |
| 30 | 497 | 88.8 | 108 | 5 | US-10-938-353-117 | Sequence 117, App |
| 31 | 494 | 88.2 | 108 | 5 | US-10-725-962-36 | Sequence 36, Appl |
| 32 | 494 | 88.2 | 108 | 5 | US-10-725-962-38 | Sequence 38, Appl |
| 33 | 494 | 88.2 | 236 | 3 | US-09-859-053-30 | Sequence 30, Appl |
| 34 | 494 | 88.2 | 236 | 4 | US-10-800-250-30 | Sequence 30, Appl |
| 35 | 494 | 88.2 | 236 | 4 | US-10-625-105-30 | Sequence 30, Appl |
| 36 | 493 | 88.0 | 107 | 5 | US-10-727-155-312 | Sequence 312, App |
| 37 | 493 | 88.0 | 108 | 4 | US-10-408-901-20 | Sequence 8, Appli |
| 38 | 493 | 88.0 | 126 | 4 | US-10-469-125-8 | Sequence 20, Appl |
| 39 | 493 | 88.0 | 129 | 5 | US-10-910-901-20 | Sequence 44, Appl |
| 40 | 493 | 88.0 | 214 | 4 | US-10-408-901-44 | Sequence 6, Appli |
| 41 | 493 | 88.0 | 233 | 5 | US-10-769-144-6 | Sequence 6, Appli |
| 42 | 493 | 88.0 | 233 | 5 | US-10-903-191-6 | Sequence 24, Appl |
| 43 | 493 | 88.0 | 234 | 4 | US-10-292-088-24 | Sequence 105, App |
| 44 | 492 | 87.9 | 107 | 4 | US-10-292-088-105 | Sequence 18, Appl |
| 45 | 492 | 87.9 | 108 | 5 | US-10-726-332-18 | |

ALIGNMENTS

RESULT 1
US-09-795-798-2
; Sequence 2, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2

Query Match 100.0%; Score 560; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 4e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPKAPKLLYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPKAPKLLYSGSTLQSGVPS 60

QY 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108
|||||
Db 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108

RESULT 2

US-10-727-737-2
; Sequence 2, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; ; Jardieu, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/727,737

FILING DATE: 03-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/975,329B

FILING DATE: 20-Nov-1997

APPLICATION NUMBER: 60/031945

FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1064R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-727-737-2

Query Match 100.0%; Score 560; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPPSSLSASVGDRTVITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60
|||||
Db 1 DIQWTSPPSSLSASVGDRTVITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108
|||||
Db 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108

RESULT 3

US-10-877-532-5

; Sequence 5, Application US/10877532

; Publication No. US20050038231A1

GENERAL INFORMATION:

; APPLICANT: FAHRNER, ROBERT L.

; APPLICANT: LAVERDIERE, AMY

; APPLICANT: MCDONALD, PAUL J.

; APPLICANT: O'LEARY, RHONA M.

; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
; FILE REFERENCE: P2015R1
; CURRENT APPLICATION NUMBER: US/10/877,532
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,500
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-5

Query Match 100.0%; Score 560; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 4e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPPSSLSASVGDRTVITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60
|||||
Db 1 DIQWTSPPSSLSASVGDRTVITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108
|||||
Db 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108

RESULT 4

US-10-423-299-3

; Sequence 3, Application US/10423299

; Publication No. US20030229212A1

GENERAL INFORMATION:

; APPLICANT: FAHRNER, ROBERT

; APPLICANT: FOLLMAN, DEBORAH

; APPLICANT: LEBRETON, BENEDICTE

; APPLICANT: VAN REIS, ROBERT

; TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS

; FILE REFERENCE: 39766-0121A

; CURRENT APPLICATION NUMBER: US/10/423,299

; CURRENT FILING DATE: 2003-04-25

; PRIOR APPLICATION NUMBER: US 60/375,953

; PRIOR FILING DATE: 2002-04-26

; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 3

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized

US-10-423-299-3

Query Match 100.0%; Score 560; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPPSSLSASVGDRTVITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60
|||||
Db 1 DIQWTSPPSSLSASVGDRTVITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108
|||||
Db 61 RFSGSGSGTDTLTITISLQPEDFATYYCQOHNEYPITFGGQTKVEIKR 108

RESULT 5

US-09-726-258-47

; Sequence 47, Application US/09726258

; Publication No. US20030021790A1

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Hsei, Vanessa

; APPLICANT: Koumenis, Iphigenia

; APPLICANT: Leong, Steven R.

```

; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P108SR4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; US-09-726-258-47

Query Match 97.6%; Score 546.5; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 5.4e-38;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKAPKLLIYSGSTLQSGVP 60

Qy 60 SRFGSGSGTDTLTITSSLPQEDPATYCCQHNVEPLTFGQGTKEIKR 108
Db 61 SRFGSGSGTDTLTITSSLPQEDPATYCCQHNVEPLTFGQGTKEIKR 109

RESULT 6
US-09-056-1608-12
; Sequence 12, Application US/090561608
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

```

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; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-056-1608-12

Query Match 90.4%; Score 506; DB 3; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISNYLAWYQKPKAPKLLIYAASLSGVP 60

Qy 61 RFSGSGSGTDTLTITSSLPQEDPATYCCQHNVEPLTFGQGTKEIKR 108
Db 61 RFSGSGSGTDTLTITSSLPQEDPATYCCQHNVEPLTFGQGTKEIKR 108

RESULT 7
US-09-795-798-3
; Sequence 3, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:

```


; Sequence 38, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-861-049-38

Query Match 90.4%; Score 506; DB 5; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Cy 1 DIQWTPSSLSASVGRVITTCRASKTISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTPSSLSASVGRVITTCRASKTISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

Cy 61 RFGSGSGTDTTLTISSLPQEDFATYCCQHNHYPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDTTLTISSLPQEDFATYCCQHNHYPLTFGQGTKEIKR 108

RESULT 11
US-10-974-591-12
Sequence 12, Application US/10974591
Publication No. US20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.

; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-974-591-12

Query Match 90.4%; Score 506; DB 5; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Cy 1 DIQWTPSSLSASVGRVITTCRASKTISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTPSSLSASVGRVITTCRASKTISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

Cy 61 RFGSGSGTDTTLTISSLPQEDFATYCCQHNHYPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDTTLTISSLPQEDFATYCCQHNHYPLTFGQGTKEIKR 108

RESULT 12
US-11-021-874-38
Sequence 38, Application US/11021874
Publication No. US20050163775A1
GENERAL INFORMATION:
APPLICANT: Andrew Chan
APPLICANT: Qian Gong
APPLICANT: Flavius Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040R1P1
CURRENT APPLICATION NUMBER: US/11/021,874
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 10/861,049
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 38
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-11-021-874-38

Query Match 90.4%; Score 506; DB 6; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Cy 1 DIQWTPSSLSASVGRVITTCRASKTISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQWTPSSLSASVGRVITTCRASKTISKYLAQQKPKAPKLLIYSGSTLQSGVPS 60

Cy 61 RFGSGSGTDTTLTISSLPQEDFATYCCQHNHYPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDTTLTISSLPQEDFATYCCQHNHYPLTFGQGTKEIKR 108

RESULT 13
US-09-811-123-6
Sequence 6, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall

```
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6

Query Match          90.4%; Score 506; DB 3; Length 109;
Best Local Similarity 89.8%; Pred. No. 1.2e-34; Indels 0; Gaps 0;
Matches 97; Conservative 6; Mismatches 5;

Qy 1 DIQWTQSPSSLSASVGDVRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTIQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVITTCRAKTIISKYLAQQKPKAPKLLIYAASSLESQVPS 60

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCQQHNEVPLTFGGQTKVEIKR 108
Db 61 RFGSGSGTDFTLTITSLQPEDFATYYCQVNSLPWTFGGQTKVEIKR 108

RESULT 14
US-10-044-896-4
; Sequence 4, Application US/10044896
; Publication No. US20030166228A1
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Jin K.
; APPLICANT: Stewart, Timothy
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
; FILE REFERENCE: GENENT.074A
; CURRENT APPLICATION NUMBER: US/10/044,896
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 60/270775
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-896-4

Query Match          90.4%; Score 506; DB 4; Length 110;
Best Local Similarity 89.8%; Pred. No. 1.3e-34; Indels 0; Gaps 0;
Matches 97; Conservative 6; Mismatches 5;

Qy 1 DIQWTQSPSSLSASVGDVRVITTCRAKTIISKYLAQQKPKAPKLLIYSGSTIQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVITTCRAKTIISKYLAQQKPKAPKLLIYAASSLESQVPS 60

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCQQHNEVPLTFGGQTKVEIKR 108
Db 61 RFGSGSGTDFTLTITSLQPEDFATYYCQVNSLPWTFGGQTKVEIKR 108

RESULT 15
US-09-809-739-10
; Sequence 10, Application US/09809739
; Patent No. US20020106369A1
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; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain variable region with signal
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-809-739-10

Query Match          90.2%; Score 505; DB 3; Length 127;
Best Local Similarity 90.7%; Pred. No. 1.7e-34; Indels 0; Gaps 0;
Matches 98; Conservative 4; Mismatches 6;

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Db 20 DIQWTQSPSSLSASVGDVRVITTCRAKSIISNYLAQQKPKAPKLLIYTGSTLRSGVPS 79

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCQQHNEVPLTFGGQTKVEIKR 108
Db 80 RFGSGSGTDFTLTITSLQPEDATYYCQYERPLTFGGQTKVEIKR 127

Search completed: April 13, 2006, 17:24:38
Job time : 107.114 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 13, 2006, 17:19:00 ; Search time 31.5983 Seconds
(without alignments)
282.578 Million cell updates/sec

Title: US-10-727-737-2
Perfect score: 560
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTFCGGTKVKEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/pCTUS-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 560 | 100.0 | 108 | 2 | US-08-974-899-2 |
| 2 | 560 | 100.0 | 108 | 2 | US-09-795-798-2 |
| 3 | 546.5 | 97.6 | 109 | 2 | US-09-027-449-47 |
| 4 | 546.5 | 97.6 | 109 | 2 | US-08-804-444A-47 |
| 5 | 546.5 | 97.6 | 109 | 2 | US-09-026-985-47 |
| 6 | 546.5 | 97.6 | 109 | 2 | US-09-121-952A-47 |
| 7 | 546.5 | 97.6 | 109 | 2 | US-09-234-340A-47 |
| 8 | 546.5 | 97.6 | 109 | 2 | US-09-355-014-47 |
| 9 | 506 | 90.4 | 108 | 2 | US-08-974-899-3 |
| 10 | 506 | 90.4 | 108 | 2 | US-09-795-798-3 |
| 11 | 505 | 90.2 | 108 | 2 | US-08-908-469-12 |
| 12 | 505 | 90.2 | 127 | 2 | US-09-809-739-10 |
| 13 | 504 | 90.0 | 109 | 1 | US-07-934-373C-3 |
| 14 | 504 | 90.0 | 109 | 2 | US-08-437-642B-3 |
| 15 | 504 | 90.0 | 109 | 2 | US-08-146-206C-3 |
| 16 | 504 | 90.0 | 109 | 2 | US-09-705-686-3 |
| 17 | 504 | 90.0 | 109 | 2 | US-09-705-392A-3 |
| 18 | 504 | 90.0 | 109 | 2 | US-09-705-398-3 |
| 19 | 504 | 90.0 | 109 | 4 | PCT-US93-07832-3 |
| 20 | 501 | 89.5 | 107 | 1 | US-07-934-373C-18 |
| 21 | 501 | 89.5 | 107 | 2 | US-08-437-642B-18 |
| 22 | 501 | 89.5 | 107 | 2 | US-08-146-206C-18 |
| 23 | 501 | 89.5 | 107 | 2 | US-09-648-067A-14 |
| 24 | 501 | 89.5 | 107 | 2 | US-09-705-686-18 |
| 25 | 501 | 89.5 | 107 | 2 | US-09-705-392A-18 |
| 26 | 501 | 89.5 | 107 | 2 | US-09-705-398-18 |
| 27 | 501 | 89.5 | 107 | 2 | US-09-602-812A-5 |

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| 28 | 501 | 89.5 | 107 | 4 | PCT-US93-07832-18 |
| 29 | 501 | 89.5 | 109 | 2 | US-09-025-769B-28 |
| 30 | 501 | 89.5 | 109 | 2 | US-09-025-769B-43 |
| 31 | 501 | 89.5 | 109 | 2 | US-09-490-070A-28 |
| 32 | 501 | 89.5 | 109 | 2 | US-09-490-070A-43 |
| 33 | 501 | 89.5 | 109 | 2 | US-09-490-153-28 |
| 34 | 501 | 89.5 | 109 | 2 | US-09-490-153-43 |
| 35 | 501 | 89.5 | 109 | 2 | US-09-490-324-28 |
| 36 | 501 | 89.5 | 109 | 2 | US-09-490-324-43 |
| 37 | 497 | 88.8 | 109 | 2 | US-09-157-370-3 |
| 38 | 494 | 88.2 | 236 | 2 | US-09-859-053-30 |
| 39 | 493 | 88.0 | 108 | 2 | US-09-025-769B-14 |
| 40 | 493 | 88.0 | 108 | 2 | US-09-490-070A-14 |
| 41 | 493 | 88.0 | 108 | 2 | US-09-490-153-14 |
| 42 | 493 | 88.0 | 108 | 2 | US-09-490-153-14 |
| 43 | 490 | 87.5 | 108 | 1 | US-08-379-057-29 |
| 44 | 490 | 87.5 | 108 | 2 | US-09-920-262A-8 |
| 45 | 490 | 87.5 | 240 | 2 | US-09-192-854-2 |

ALIGNMENTS

RESULT 1
US-08-974-899-2
; Sequence 2, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-974-899-2

Query Match 100.0%; Score 560; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWQKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWQKPGKAPKLLIYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDTLTITSSLPEDFATYYCQOHNEYPITFGQGTVEIKR 108
 |||||
 Db 61 RFGSGSGTDTLTITSSLPEDFATYYCQOHNEYPITFGQGTVEIKR 108

RESULT 2

US-09-795-798-2
 ; Sequence 2, Application US/09795798
 ; Patent No. 6703018
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; ; Jardieu, Paula M.
 ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/795,798
 ; FILING DATE: 28-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/974,899
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P1014R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 2:
 ; LENGTH: 108 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-795-798-2

Query Match 100.0%; Score 560; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 7e-42;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSLASVGRVITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
 |||||
 Db 1 DIQWTQSPSLASVGRVITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDTLTITSSLPEDFATYYCQOHNEYPITFGQGTVEIKR 108
 |||||
 Db 61 RFGSGSGTDTLTITSSLPEDFATYYCQOHNEYPITFGQGTVEIKR 108

RESULT 3

US-09-027-449-47
 ; Sequence 47, Application US/09027449
 ; Patent No. 6025158
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania R.
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/027,449
 ; FILING DATE: 20-Feb-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/074,330
 ; FILING DATE: 22-Jan-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/038,664
 ; FILING DATE: 21-Feb-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P1085R3-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 47:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 109 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-09-027-449-47

Query Match 97.6%; Score 546.5; DB 2; Length 109;
 Best Local Similarity 98.2%; Pred. No. 1.1e-40;
 Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQWTQSPSLASVGRVITTCRASTISKYLAWYQKPKAPKLLI-YSGSTLQSGVP 59
 |||||
 Db 1 DIQWTQSPSLASVGRVITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVP 60

Qy 60 SRFGSGSGTDTLTITSSLPEDFATYYCQOHNEYPITFGQGTVEIKR 108
 |||||
 Db 61 SRFGSGSGTDTLTITSSLPEDFATYYCQOHNEYPITFGQGTVEIKR 109

RESULT 4

US-08-804-444A-47
 ; Sequence 47, Application US/0880444A
 ; Patent No. 6117980
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania N
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/804,444A
 ; FILING DATE: 21-Feb-1997

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-804-444A-47

Query Match 97.6%; Score 546.5; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.1e-40;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAWYQKPGKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVP 60

Qy 60 SRFGSGSGTDTLTITSSLPEDPATYTCQOHNEYPITFGQGTKEIKR 108
Db 61 SRFGSGSGTDTLTITSSLPEDPATYTCQOHNEYPITFGQGTKEIKR 109

RESULT 5
US-09-026-985-47
Sequence 47, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-47

Query Match 97.6%; Score 546.5; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.1e-40;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAWYQKPGKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVP 60

Qy 60 SRFGSGSGTDTLTITSSLPEDPATYTCQOHNEYPITFGQGTKEIKR 108
Db 61 SRFGSGSGTDTLTITSSLPEDPATYTCQOHNEYPITFGQGTKEIKR 109

RESULT 6
US-09-121-952A-47
Sequence 47, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-47

Query Match 97.6%; Score 546.5; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.1e-40;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAWYQKPGKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVP 60

Qy 60 SRFGSGSGTDTLTITSSLPEDPATYTCQOHNEYPITFGQGTKEIKR 108
Db 61 SRFGSGSGTDTLTITSSLPEDPATYTCQOHNEYPITFGQGTKEIKR 109

RESULT 7

US-09-234-340A-47
; Sequence 47, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-234-340A-47
Query Match 97.6%; Score 546.5; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.1e-40;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKPKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKPKAPKLLIYYSGSTLQSGVP 60
Qy 60 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPITFGGKTKVEIKR 108
Db 61 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPITFGGKTKVEIKR 109
RESULT 8
US-09-355-014-47
; Sequence 47, Application US/09355014
; Patent No. 6870033
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.

Shahrokhi, Zahra
Zapata, Gerardo A.
Humanized Anti-IL-8 Monoclonal Antibodies
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-355-014-47
Query Match 97.6%; Score 546.5; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.1e-40;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKPKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKPKAPKLLIYYSGSTLQSGVP 60
Qy 60 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPITFGGKTKVEIKR 108
Db 61 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPITFGGKTKVEIKR 109
RESULT 9
US-08-974-899-3
; Sequence 3, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:

```

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-974-899-3

Query Match 90.4%; Score 506; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. NO. 3.6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Cy 1 DIQMTQSPSSLSASVGDRTVITTCRAKSTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQISINYLAWYQKPGKAPKLLIYAASLSGVS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDFATYYCQHNHYPLTFGGTKVEIKR 108
Db 61 RFSGSGGTDTFTLTISLQPEDFATYYCQYNSLPWTFGGTKVEIKR 108

RESULT 10
US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-795-798-3
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Query Match 90.4%; Score 506; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. NO. 3.6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRAKSTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQISINYLAWYQKPGKAPKLLIYAASLSGVS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDFATYYCQHNHYPLTFGGTKVEIKR 108
Db 61 RFSGSGGTDTFTLTISLQPEDFATYYCQYNSLPWTFGGTKVEIKR 108

RESULT 11
US-08-908-469-12
; Sequence 12, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-08-908-469-12
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Query Match 90.4%; Score 506; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. NO. 3.6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRAKSTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQISINYLAWYQKPGKAPKLLIYAASLSGVS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDFATYYCQHNHYPLTFGGTKVEIKR 108
Db 61 RFSGSGGTDTFTLTISLQPEDFATYYCQYNSLPWTFGGTKVEIKR 108
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```
RESULT 12
US-09-809-739-10
; Sequence 10, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain variable region with signal
; OTHER INFORMATION: sequence
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-809-739-10

Query Match          90.2%; Score 505; DB 2; Length 127;
Best Local Similarity 90.7%; Pred. No. 5.2e-37;
Matches 98; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASTISKYLAWYQOKPGKAPKLLIYSGSTIQSGVPS 60
   |||||
Db 20 DIQMTQSPSSLSASVGRVITTCRASTISKYLSINLAWYQOKPGKAPKLLIYSGSTLRSGVPS 79
   |||||

Qy 61 RFGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGQGTKVEIKR 108
   |||||
Db 80 RFGSGSGTDFTLTISLQPEDPATYTCQQYVERPLTFGQGTKVEIKR 127
   |||||

RESULT 13
US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER:
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION NUMBER:
; FILING DATE: 07/715272
; APPLICATION NUMBER:
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino acid
; NAME: Lee, Wendy M.
```

```
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-3

Query Match          90.0%; Score 504; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 5.4e-37;
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASTISKYLAWYQOKPGKAPKLLIYSGSTIQSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVITTCRASTISQDVSSYLAWYQOKPGKAPKLLIYAAASLESQVPS 60
   |||||

Qy 61 RFGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGQGTKVEIKR 108
   |||||
Db 61 RFGSGSGTDFTLTISLQPEDPATYTCQQYNSLPTFTFGQGTKVEIKR 108
   |||||

RESULT 14
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino acid
; NAME: Lee, Wendy M.
```

```

; TOPOLOGY: Linear
US-08-437-642B-3
Query Match 90.0%; Score 504; DB 2; Length 109;
Best Local Similarity 88.9%; Pred. No. 5.4e-37;
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDVSSYLAWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFGSGSGTDFTLTISSLPQDPFATYCCQHNVEPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDFTLTISSLPQDPFATYCCQHNVEPLTFGQGTKEIKR 108

```

```

RESULT 15
US-08-146-206C-3
Sequence 3, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-3

```

```

Query Match 90.0%; Score 504; DB 2; Length 109;
Best Local Similarity 88.9%; Pred. No. 5.4e-37;
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDVSSYLAWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFGSGSGTDFTLTISSLPQDPFATYCCQHNVEPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDFTLTISSLPQDPFATYCCQHNVEPLTFGQGTKEIKR 108

```

Search completed: April 13, 2006, 17:20:47
Job time : 32.5983 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 17:05:54 ; Search time 140.07 Seconds
(without alignments)
543.993 Million cell updates/sec

Title: US-10-727-737-2

Perfect score: 560

Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTFQGQTKVKEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt.05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|--------------|--------------------|
| 1 | 486 | 86.8 | 236 | 2 | Q6GMX8 HUMAN | Q6gmX8 homo sapien |
| 2 | 481 | 85.9 | 108 | 1 | KV1V HUMAN | P04430 homo sapien |
| 3 | 481 | 85.9 | 236 | 2 | Q7Z3Y4 HUMAN | Q7z3Y4 homo sapien |
| 4 | 479 | 85.5 | 108 | 2 | Q9UL70 HUMAN | Q9ul70 homo sapien |
| 5 | 479 | 85.5 | 236 | 2 | Q6GMX9 HUMAN | Q6gmX9 homo sapien |
| 6 | 478 | 85.4 | 236 | 2 | Q6PIH7 HUMAN | Q6piH7 homo sapien |
| 7 | 476 | 85.0 | 236 | 2 | Q6GMW1 HUMAN | Q6gmW1 homo sapien |
| 8 | 475 | 84.8 | 108 | 1 | KV1H HUMAN | Q9ul77 homo sapien |
| 9 | 474 | 84.6 | 108 | 1 | Q9UL77 HUMAN | P01600 homo sapien |
| 10 | 473.5 | 84.6 | 107 | 2 | Q96SA9 HUMAN | Q96sa9 homo sapien |
| 11 | 471 | 84.1 | 236 | 2 | Q502W4 HUMAN | Q502w4 homo sapien |
| 12 | 471 | 84.1 | 244 | 2 | Q6SZC8 HUMAN | Q6szC8 homo sapien |
| 13 | 470 | 83.9 | 240 | 2 | Q6SZC9 HUMAN | Q6szC9 homo sapien |
| 14 | 464 | 82.9 | 108 | 1 | KV1M HUMAN | P01605 homo sapien |
| 15 | 463 | 82.7 | 234 | 2 | Q7Z473 HUMAN | Q7z473 homo sapien |
| 16 | 463 | 82.7 | 236 | 2 | Q6GMX0 HUMAN | Q6gmX0 homo sapien |
| 17 | 462 | 82.5 | 108 | 2 | Q9UL79 HUMAN | Q9ul79 homo sapien |
| 18 | 461 | 82.3 | 108 | 1 | KV1G HUMAN | P01599 homo sapien |
| 19 | 461 | 82.3 | 108 | 1 | KV1L HUMAN | P01604 homo sapien |
| 20 | 460 | 82.1 | 108 | 1 | KV1S HUMAN | P01611 homo sapien |
| 21 | 459.5 | 81.9 | 107 | 1 | KV1D HUMAN | P01596 homo sapien |
| 22 | 458 | 81.8 | 108 | 1 | KV1B HUMAN | P01594 homo sapien |
| 23 | 458 | 81.8 | 129 | 1 | KV1W HUMAN | P04431 homo sapien |
| 24 | 456 | 81.4 | 236 | 2 | Q6PII5 HUMAN | Q6piI5 homo sapien |
| 25 | 455 | 81.2 | 108 | 1 | KV1F HUMAN | P01598 homo sapien |
| 26 | 455 | 81.2 | 108 | 1 | KV1O HUMAN | P01607 homo sapien |
| 27 | 455 | 81.2 | 108 | 1 | KV1R HUMAN | P01610 homo sapien |
| 28 | 452 | 80.7 | 108 | 1 | KV1N HUMAN | P01606 homo sapien |
| 29 | 452 | 80.7 | 108 | 1 | KV1P HUMAN | P01608 homo sapien |
| 30 | 452 | 80.7 | 108 | 1 | KV1Y HUMAN | P00362 homo sapien |
| 31 | 451.5 | 80.6 | 107 | 2 | Q9UL81 HUMAN | Q9ul81 homo sapien |

RESULT 1

Q6GMX8 HUMAN

ID Q6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6GMX8;

DT 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE IGKC protein.

OS Name=IGKC;

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udgin T.B., Toshyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RG NIH MGC Project;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073764; AAH73764.1; -; mRNA.

DR SMR; Q6GMX8; 24-235.

DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG.cl.

DR InterPro; IPR003006; IG.MHC.

DR InterPro; IPR003596; IG.v.

DR Pfam; PF07654; CI-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

| | | | | | | |
|----|-------|------|-----|---|--------------|--------------------|
| 32 | 450 | 80.4 | 108 | 1 | KV1K HUMAN | P01603 homo sapien |
| 33 | 449 | 80.2 | 236 | 2 | Q6PIH4 HUMAN | Q6piH4 homo sapien |
| 34 | 447 | 79.8 | 108 | 1 | KV1E HUMAN | P01597 homo sapien |
| 35 | 447 | 79.8 | 108 | 1 | KV1Q HUMAN | P01609 homo sapien |
| 36 | 443 | 79.1 | 234 | 2 | Q5EFE6 HUMAN | Q5efe6 homo sapien |
| 37 | 442 | 78.9 | 189 | 2 | Q56917 HUMAN | Q56917 homo sapien |
| 38 | 439 | 78.4 | 108 | 1 | KV1A HUMAN | P01593 homo sapien |
| 39 | 434 | 77.5 | 129 | 1 | KV1X HUMAN | P04432 homo sapien |
| 40 | 432 | 77.1 | 117 | 1 | KV1J HUMAN | P01602 homo sapien |
| 41 | 431 | 77.0 | 117 | 1 | KV1I HUMAN | P01601 homo sapien |
| 42 | 430 | 76.8 | 108 | 1 | KV1C HUMAN | P01595 homo sapien |
| 43 | 428 | 76.4 | 116 | 2 | Q6PPE6 HUMAN | Q6ppe6 homo sapien |
| 44 | 423.5 | 75.6 | 109 | 1 | KV1T HUMAN | P01612 homo sapien |
| 45 | 412 | 73.6 | 108 | 1 | KV5D_MOUSE | P01636 mus musculu |

ALIGNMENTS

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 86.8%; Score 486; DB 2; Length 236;
Best Local Similarity 86.1%; Pred. No. 1.9e-41;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVVTITCRASKTISKYLAWYQKQKPKLIYSGTSLQSGVPS 60
Db 23 DIQWTQSPSSLSASVGRVVTITCRASGIGISLAWYQKQKPKLIYRASSLQSGVPS 82
QY 61 RFGSGSGTDTLTITISSLPQEDPATYCYCOQHNEYPLTFGGTKVIEKR 108
Db 83 RFGSGSGTDTLTITISSLPQEDPATYCYCOQHNSFPFTFGPTKVDIEKR 130

RESULT 2
KVIV_HUMAN KVIV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwalet P.E., O'Connor T.P., Benson M.D.;
RL "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
MOl. Immunol. 23:73-78(1986).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTL.
DR SNR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 85.9%; Score 481; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 2.5e-41;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVVTITCRASKTISKYLAWYQKQKPKLIYSGTSLQSGVPS 60

```

Db 83 KPSGSGTGDTLTITSSLOPEDPATYCCQYKSPVTFQGTKLKIKR 130

RESULT 4

Q9UL70 HUMAN

ID Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.

AC Q9UL70

DE 01-MAY-2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DI 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

CC Homo.

CC NCBI_TaxID=9606;

EN [1]

EP NUCLEOTIDE SEQUENCE.

EX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

EA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

EA Young D.C.;

ET "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".

ET Clin. Immunol. Immunopathol. 87:184-192(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=1660528;

RZ Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,

RA Diamond B.;

RT "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype".

RT J. Exp. Med. 174:1639-1652(1991).

DR EMBL; AF035044; AAD56280.1; -; mRNA.

DR PIR; PH0863; PH0863.

DR HSP; P01607; 1BMW.

DR SMR; Q9UL70; 1-108.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 1.

FT NON_TER 1

FT NON_TER 108

SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 85.5%; Score 479; DB 2; Length 108;

Best Local Similarity 86.1%; Pred. No. 4e-41;

Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAQQKPGKAPKLLIYSGTQSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNLYLAQQKPGKPKSLIYAASLTQSGVPS 60

QY 61 RPSGSGGTDFLTITSSLOPEDPATYCCQYKSPVTFQGTKLKIKR 108

Db 61 RPSGSGGTDFLTITSSLOPEDPATYCCQYKSPVTFQGTKLKIKR 108

RESULT 5

Q6GKX9 HUMAN

ID Q6GKX9 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6GKX9;

DE 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DI 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE IGKC protein.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

CC Homo.

CC NCBI_TaxID=9606;

EN [1]

RP NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Hapkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RX NIH MGC Project;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073763; AAH73763.1; -; mRNA.

DR SMR; Q6GKX9; 23-236.

DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG MHC; UNKNOWN 1.

SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF77 CRC64;

Query Match 85.5%; Score 479; DB 2; Length 236;

Best Local Similarity 85.2%; Pred. No. 9.9e-41;

Matches 92; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAQQKPGKAPKLLIYSGTQSGVPS 60

Db 23 DIQMTQSPSSLSASVGHRTVITCRASQNSRSLAYQQRPEKAPKSLIYATSLHSGVPS 82

QY 61 RPSGSGGTDFLTITSSLOPEDPATYCCQYKSPVTFQGTKLKIKR 108

Db 83 RPSGSGGTDFLTITSSLOPEDPATYCCQYKSPVTFQGTKLKIKR 130

RESULT 6

Q6PIH7 HUMAN

ID Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH7;

DE 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DI 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE IGKC protein.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

CC Homo.

CC NCBI_TaxID=9606;

EN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC034141; AAH34141.1; -, mRNA.
 DR HSP; P01607; 1A2.
 DR SMR; Q6PIH7; 23-236.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
 Query Match 85.4%; Score 478; DB 2; Length 236;
 Best Local Similarity 87.0%; Pred. No. 1.3e-40;
 Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 DIQWTSPLSASVGDRTTTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
 Db 23 DIQLTQSPFLSASVGDRTTTCRASQGISYLAWYQKPKAPNLLIYAASTLQSGVPS 82
 Qy 61 RFGSGSGTDTLTITSLQPEDFATYCCQHNEVPLTFGGTKVEIKR 108
 Db 83 RFGSGSGTDTLTITSLQPEDFATYCCQLNSPPTFGGTKVEIKR 130
 RESULT 7
 Q6GMW1_HUMAN
 ID Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q6GMW1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC073791; AAH73791.1; -, mRNA.
 DR SMR; Q6GMW1; 24-236.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087AFAC437 CRC64;
 Query Match 85.0%; Score 476; DB 2; Length 236;
 Best Local Similarity 87.9%; Pred. No. 2e-40;
 Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 Qy 2 IQMTQSPSSLASVGDRTTTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPSR 61
 Db 24 IQMTQSPSSLASVGDRTTTCRASQGISNDLWYQKPKAPKLLIYAASSLQSGVPSR 83
 Qy 62 FSGSGSGTDTLTITSLQPEDFATYCCQHNEVPLTFGGTKVEIKR 108
 Db 84 FSGSGSGTDTLTITSLQPEDFATYCCQDYNVPTFGGTKVEIKR 130
 RESULT 8
 Q9UL77_HUMAN
 ID Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
 AC Q9UL77;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

```

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RA fetus."
RA Clin. Immunol. Immunopathol. 87:184-192(1998).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal striational autoantibodies isolated from thymic B
RA lymphocytes of patients with myasthenia gravis use VH and VL gene
RA segments associated with the autoimmune repertoire."
RL Eur. J. Immunol. 22:2231-2236(1992).
RL [3]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RA distributed over a large portion of the V kappa locus and do not show
RA somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RL EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS0835; IG_LIKE; 1.
DR NON TER 1
DR NON TER 108
DR NON TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 84.8%; Score 475; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 1e-40;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTTTCRASKTISKYLAWYQKPGKAPKLLYSGSTLQSGVPS 60
Db 1 DIQMTSPSSLSASVGDRTTTCRASKTISKYLAWYQKPGKAPKLLYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDTLTITSSLPDEPFIYCOQNEVPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDTLTITSSLPDEPFIYCOQNEVPLTFGQGTKEIKR 108

RESULT 9
KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RA "The primary structure of a monoclonal kappa-type immunoglobulin L-
RA chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RA subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01868; K1HUHU.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 84.6%; Score 474; DB 1; Length 108;
Best Local Similarity 84.3%; Pred. No. 1.3e-40;
Matches 91; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTTTCRASKTISKYLAWYQKPGKAPKLLYSGSTLQSGVPS 60
Db 1 DIQMTSPSSLSASVGDRTTTCRASKTISKYLAWYQKPGKAPKLLYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDTLTITSSLPDEPFIYCOQNEVPLTFGQGTKEIKR 108
Db 61 RFGSGSGTDTLTITSSLPDEPFIYCOQNEVPLTFGQGTKEIKR 108

RESULT 10
Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RA "Molecular analysis of polyclonal monoclonal antibodies from
RA rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RA antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal striational autoantibodies isolated from thymic B
RA lymphocytes of patients with myasthenia gravis use VH and VL gene
RA segments associated with the autoimmune repertoire."
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;

```

RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation."; [4]
 RL Eur. J. Immunol. 23:391-397(1993).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1660528;
 RA Diamond B.; characteristics of antibodies bearing an anti-DNA-
 RA associated idiotype."; [5]
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idiotype."; [5]
 RL J. Exp. Med. 174:1639-1652(1991).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1903706;
 RA Blais G., Kuntz J.L., Pasquali J.L.;
 RT "Molecular analysis of V kappa III variable regions of polyclonal
 RT rheumatoid factors during rheumatoid arthritis."; [4]
 RL Eur. J. Immunol. 21:1221-1227(1991).
 DR EMBL: U96396; AAB68785.1; -; mRNA.
 DR PIR: B49047; B49047.
 DR PIR: PH0867; PH0867.
 DR PIR: S16840; S16840.
 DR PIR: S31977; S31977.
 DR PIR: S34083; S34083.
 DR PIR: S34086; S34086.
 DR HSP: P01607; 1BWW.
 DR SMR: Q96SA9; 1-107.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1 107
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 84.6%; Score 473.5; DB 2; Length 107;
 Best Local Similarity 88.0%; Pred. No. 1.5e-40;
 Matches 95; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
 Qy 1 DIQWQPSLSASVGRVITTCRAKTIISKYLAQYQKPKAPKLLIYSGSTLQSGVPS 60
 Db 1 DIQWQPSLSASVGRVITTCRAKTIISKYLAQYQKPKAPKLLIYSGSTLQSGVPS 60
 Qy 61 RFGSGSGTDTLTITSLQPEDFATYCCQHNEYPFTFGGQTKVEIKR 108
 Db 61 RFGSGSGTDTLTITSLQPEDFATYCCQHNEYPFTFGGQTKVEIKR 107

RESULT 11
 Q502M4_HUMAN
 ID Q502M4_HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q502M4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Glandular pool- thyroid;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
 RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; [2]
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Glandular pool- thyroid;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC095489; AAH95489.1; -; mRNA.
 DR SMR: Q502M4; 23-236.
 DR Ensembl: ENSG00000163245; Homo sapiens.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF07654; Cl-set; 1.
 DR SMART: SM00409; IGV; 2.
 DR SMART: SM00406; IGV; 1.
 DR SMART: SM00407; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 84.1%; Score 471; DB 2; Length 236;
 Best Local Similarity 84.3%; Pred. No. 6.6e-40;
 Matches 91; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 DIQWQPSLSASVGRVITTCRAKTIISKYLAQYQKPKAPKLLIYSGSTLQSGVPS 60
 Db 23 DIQWQPSLSASVGRVITTCRAKTIISKYLAQYQKPKAPKLLIYSGSTLQSGVPS 82
 Qy 61 RFGSGSGTDTLTITSLQPEDFATYCCQHNEYPFTFGGQTKVEIKR 108
 Db 83 RFGSGSGTDTLTITSLQPEDFATYCCQHNEYPFTFGGQTKVEIKR 130

RESULT 12
 Q65ZC8_HUMAN
 ID Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
 AC Q65ZC8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies."; [4]
 RL Nat. Biotechnol. 15:629-631(1997).
 DR EMBL: Y13057; CAA73500.1; -; mRNA.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.

```

DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 1
FT NON TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match      84.1%; Score 471; DB 2; Length 244;
Best Local Similarity 82.4%; Pred. No. 6.8e-40;
Matches 89; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 DIQMTQSPSTLSASIGRVTITCRASEGIYHLWYQOKPGKAPFLYIKASSLASGAPS 196
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Cy 61 RFGSGSGTDFTLTISLQPDFAFYCCQHNEYPFLTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 197 RFGSGSGTDFTLTISLQPDFAFYCCQYSNYPFLTFGGGTKEIKR 244
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
Q652C9 HUMAN
-D Q652C9 HUMAN PRELIMINARY; PRT; 240 AA.
AC Q652C9;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
CX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 1
FT NON TER 240
SQ SEQUENCE 240 AA; 25569 MW; PDCFD3645F64B373 CRC64;

Query Match      83.9%; Score 470; DB 2; Length 240;
Best Local Similarity 82.4%; Pred. No. 8.5e-40;
Matches 89; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 133 DIQMTQSPSTLSASIGRVTITCRASEGIYHLWYQOKPGKAPKLLIYKASSLASRAPS 192
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFGSGSGTDFTLTISLQPDFAFYCCQHNEYPFLTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 193 RFGSGSGTDFTLTISLQPDFAFYCCQYSNYPFLTFGGGTKEIKR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
KVIM HUMAN
ID KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Ig kappa chain V-I region Lay.

```

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OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human Igm
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
RN [2]
RP PROTEIN SEQUENCE OF 1-104.
RX MEDLINE=89215279; PubMed=2496160;
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
Carson D., Solomon A., Mendez E., Frangione B.;
RT "Structural and idiotypic characterization of the L chains of human
IGM autoantibodies with different specificities.";
RL J. Immunol. 142:3158-3163(1989).
RN [3]
RP ERRATUM.
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
Carson D., Solomon A., Mendez E., Frangione B.;
RL J. Immunol. 143:3864-3864(1989).
CC -I- MISCELLANEOUS: The second and third hypervariable regions of this
chain are identical with those of the human POM V-III kappa chain,
with which it shares certain idiotypic determinants.
CC -I- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma
globulin activity.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
DR PIR; A01871; KIHULY.
DR HSSP; P01607; 1BWW.
DR SMR; P01605; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.

Query Match      82.9%; Score 464; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 1.4e-39;
Matches 87; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSVSGRVTITCASNVAIYLNWYQOKPGKAPKLLIYIGASTRAGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFGSGSGTDFTLTISLQPDFAFYCCQHNEYPFLTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISLQPDFAFYCCQYNNPPTFGQGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 15
Q72473 HUMAN
ID Q72473 HUMAN PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boesak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.*;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -; mRNA.
DR HSP; P01834; 1HEZ.
DR SMR; Q72473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

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Query Match      82.7%; Score 463; DB 2; Length 234;
Best Local Similarity 83.2%; Pred. No. 4.3e-39;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY      2 IQWTQSPSSLASVGDVRTITCRASKTISKYLAWYQKPKAPKLLIYSGSTLQSGVPSR 61
Db      22 IRMTQSPSSFSASTGDRVTITCRASIGSYLAWYQKPKAPOLLIIYAATLQSGVPSR 81

QY      62 FSGSGSGTDFTLTISSLPQEDFATFYCQHNNEYPFLTFGQGTKVEIKR 108
Db      82 FSGSASGTDFTLSISCLQSDFAFYCQYYTYEYPTWTFGQGTKVEIKR 128

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Search completed: April 13, 2006, 17:18:41
Job time : 141.07 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 17:14:06 ; Search time 23.1092 Seconds
(without alignments)
449.666 Million cell updates/sec

Title: US-10-727-737-2
Perfect score: 560
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTFGQGTKVEIKR 108
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 493 | 88.0 | 125 | 2 S40333 | Ig kappa chain V-J |
| 2 | 490 | 87.5 | 108 | 2 B49047 | Ig kappa chain V r |
| 3 | 490 | 87.5 | 129 | 2 S40369 | Ig kappa chain - h |
| 4 | 489 | 87.3 | 117 | 2 S46371 | Ig kappa chain V-J |
| 5 | 487 | 87.0 | 125 | 2 S40349 | Ig kappa chain V-J |
| 6 | 487 | 87.0 | 127 | 2 S40367 | Ig kappa chain V-J |
| 7 | 486 | 86.8 | 108 | 2 S19674 | Ig kappa chain V r |
| 8 | 486 | 86.8 | 123 | 2 S40331 | Ig kappa chain - h |
| 9 | 485 | 86.8 | 131 | 2 S40352 | Ig kappa chain V-J |
| 10 | 484.5 | 86.5 | 124 | 2 S40336 | Ig kappa chain V-J |
| 11 | 483 | 86.2 | 107 | 2 S36284 | Ig lambda chain V |
| 12 | 483 | 86.2 | 132 | 2 S40334 | Ig kappa chain - h |
| 13 | 481 | 85.9 | 108 | 1 KIHURN | Ig kappa chain V-I |
| 14 | 479 | 85.5 | 128 | 2 S46372 | Ig light chain var |
| 15 | 478 | 85.4 | 107 | 2 T59017 | anti-HIV1 envelope |
| 16 | 476.5 | 85.1 | 107 | 2 S36275 | Ig lambda chain V |
| 17 | 476 | 85.0 | 117 | 2 S46376 | Ig kappa chain V-J |
| 18 | 474 | 84.6 | 108 | 1 KIHURU | Ig kappa chain V-I |
| 19 | 474 | 84.6 | 108 | 2 S36277 | Ig lambda chain V |
| 20 | 474 | 84.6 | 132 | 2 S38646 | Ig kappa chain V r |
| 21 | 473 | 84.5 | 106 | 2 S26345 | Ig light chain V r |
| 22 | 473 | 84.5 | 109 | 2 S31998 | Ig kappa chain - h |
| 23 | 473 | 84.5 | 125 | 2 S40353 | Ig kappa chain V-J |
| 24 | 473 | 84.5 | 127 | 2 S04574 | Ig kappa chain pre |
| 25 | 472 | 84.3 | 108 | 2 S44132 | Ig kappa chain V r |
| 26 | 471 | 84.1 | 124 | 2 S40318 | Ig kappa chain V r |
| 27 | 469 | 83.8 | 125 | 2 S40316 | Ig kappa chain - h |
| 28 | 467.5 | 83.5 | 108 | 2 S30521 | Ig kappa chain V r |
| 29 | 466 | 83.2 | 108 | 2 S36279 | Ig lambda chain V |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 466 | 83.2 | 108 | 2 S47182 | Ig kappa chain - h |
| 31 | 465 | 83.0 | 109 | 2 S31981 | Ig kappa chain - h |
| 32 | 465 | 83.0 | 129 | 2 S52793 | Ig kappa chain V r |
| 33 | 464 | 82.9 | 107 | 2 S36269 | Ig lambda chain V |
| 34 | 464 | 82.9 | 108 | 1 KIHULY | Ig kappa chain V-I |
| 35 | 463.5 | 82.8 | 108 | 2 S34007 | Ig kappa chain V r |
| 36 | 462.5 | 82.6 | 107 | 2 S47183 | Ig kappa chain - h |
| 37 | 462 | 82.5 | 122 | 2 S40370 | Ig kappa chain - h |
| 38 | 462 | 82.5 | 125 | 2 S40350 | Ig kappa chain - h |
| 39 | 462 | 82.5 | 127 | 2 S11240 | Ig kappa chain V r |
| 40 | 461 | 82.3 | 108 | 1 KIHUGL | Ig kappa chain V-I |
| 41 | 461 | 82.3 | 108 | 1 KIHUKU | Ig kappa chain V-I |
| 42 | 461 | 82.3 | 129 | 2 S52789 | Ig kappa chain V r |
| 43 | 460 | 82.1 | 108 | 1 KIHUMS | Ig kappa chain V-I |
| 44 | 460 | 82.1 | 108 | 2 I39154 | Ig kappa chain (BR |
| 45 | 460 | 82.1 | 120 | 2 S46370 | Ig kappa chain V-J |

ALIGNMENTS

RESULT 1

S40333
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;Status: Preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:9441354; PIDN:CAAS1111.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 493; DB 2; Length 125;
Best Local Similarity 86.9%; Pred. No. 3.2e-34;
Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

| | | | |
|----|----|---|-----|
| Qy | 1 | DIQMTQSPSSLSASVGRVTITCRASKTISKILAWYQOKPGKAPKLLIYSGTSGVPS | 60 |
| Db | 19 | DIQMTQSPSTLSASVGRVTITCRASQSISSSLAWYQOKPGKAPKLLIYKASSLSGVS | 78 |
| Qy | 61 | RFSGSGGTDTLTITSSLOPEDATYTCQOHNEVPLTFGQGTKVEIK | 107 |
| Db | 79 | RFSGSGGTETFLTITSSLPDDFATYTCQYNSYPWTFTGQGTKVEIK | 125 |

RESULT 2

B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: Preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 490; DB 2; Length 108;
Best Local Similarity 88.9%; Pred. No. 5e-34;
Matches 96; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDVRVITTCRAKNTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQWTQSPSSLSASVGDVRVITTCRASQISISYLNWYQOKPGKAPKLLIYAASLSLQSGVPS 60
QY 61 RFSGSGSGTDFTLTITISLQPEDPATYCYCOQHNEYPLTFGGQTKVEIKR 108
DB 61 RFSGSGSGTDFTLTITISLQPEDPATYCYCOQSYSTPLTFGGGTKVEIKR 108

RESULT 3
S40369
IG kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R;Klein, R.; Jaenichen, R.; Zachau, H. G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PT
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 490; DB 2; Length 129;
Best Local Similarity 86.1%; Pred. No. 5.9e-34;
Matches 93; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDVRVITTCRAKNTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 22 DIQWTQSPSSLSASVGDVRVITTCRAKSHVISNHLVWFQOKPGKAPKSLIYAASLSLQSGVPS 81
QY 61 RFSGSGSGTDFTLTITISLQPEDPATYCYCOQHNEYPLTFGGQTKVEIKR 108
DB 82 KFSGSGSGTDFTLTITISLQPEDPATYCYCOQNSPYTFGGQTKLEIKR 129

RESULT 4
S46371
IG kappa chain V-J region (724-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S33645
R;Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: UNIPARC:UPI0000116534; EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PT
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 87.3%; Score 489; DB 2; Length 117;
Best Local Similarity 85.5%; Pred. No. 6.5e-34;
Matches 94; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIQWTQSPSSLSASVGDVRVITTCRAKNTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 8 DIQWTQSPSSLSASVGDVRVITTCRASRSISTWLNWYQOKPGKAPKLLIYKASTLESQVPS 67
QY 61 RFSGSGSGTDFTLTITISLQPEDPATYCYCOQHNEY--PLTFGGQTKVEIKR 108

Db 68 RFGSGSGGTFTLTISLQPDGFATYCCQYNYPFPYTFGGQTKLEIKR 117

RESULT 5

S40349

Ig kappa chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C/Accession: S40349

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40349

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-125 <KLE>

A/Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:9441386; PIDN:CAAS1127.1; PII:PII1127.1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 487; DB 2; Length 125;

Best Local Similarity 88.8%; Pred. No. 1e-33;

Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPSR 61

DB 19 IQLTQSPSSLSASVGRVTITCRASQGISALAWYQOKPGKAPKLLIYDASSLESQVPSR 78

QY 62 FSGSGSGTDFTLTSSLOPEDFATYCCQHNIEYPLTFGGQTKVEIKR 108

DB 79 FSGSGSGTDFTLTSSLOPEDFATYCCQFNITYPLTFGGQTKVEIKR 125

RESULT 6

S40367

Ig kappa chain V-J-C region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40367

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40367

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-127 <KLE>

A/Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 487; DB 2; Length 127;

Best Local Similarity 88.0%; Pred. No. 1e-33;

Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60

DB 18 DIQMTQSPSSLSASVGRVTITCRASQGISALAWYQOKPGKAPKLLIYAASSLQSGVPS 77

QY 61 RFGSGSGTDFTLTISLQPDGFATYCCQHNIEYPLTFGGQTKVEIKR 108

DB 78 RFGSGSGTDFTLTISLQPDGFATYCCQSYNTPTWTFGGQTKVEIKR 125

RESULT 7

S19674

Ig kappa chain V region (clone alpha-TEL9) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19674

R-Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19674

A:Molecule type: mRNA

A:Residues: 1-108 <VAR>

A:Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:PI000000000

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 486; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.1e-33;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Cy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQQKPKAPKLLIYGSTLTSGVPS 60
Db 1 ELIVLTQSPSSLASVGRVTITCRASSISNYLNWYQQKPKAPKLLIYAASLTSGVPS 60
Qy 61 RFGSGSGTDFTLTISIQLPEDPATYYCQOHNEYPPLTFGGGTKEIKR 108
Db 61 RFGSGSGTDFTLTINSLQPDPATYYCQQTNSPFLTFGGGTKEIKR 108

RESULT 8

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40331

R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDN:CAAS1109.1; PI000000000

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 486; DB 2; Length 123;
Best Local Similarity 88.8%; Pred. No. 1.2e-33;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Cy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQQKPKAPKLLIYGSTLTSGVPS 60
Db 17 DIQMTQSPSSLSASVGRVTITCRASSISNYLNWYQQKPKAPKLLIYAASLTSGVPS 76
Qy 61 RFGSGSGTDFTLTISIQLPEDPATYYCQOHNEYPPLTFGGGTKEIK 107
Db 77 RFGSGSGTDFTLTINSLQPDPATYYCQQSYPSTPTFGGTKEIK 123

RESULT 9

S40352

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40352

R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40352

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:g441392; PIDN:CAAS1130.1; PI000000000

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 486; DB 2; Length 131;
Best Local Similarity 87.0%; Pred. No. 1.3e-33;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYGSGTLQSGVPS 60
Db 21 DIQWTQSPSSLSASVGNRVTTICRASQGISNLYAWYQQKPGKVPKLLIIYAASTLQSGVPS 80

Qy 61 RFGSGSGTDFTLTISSLQPEDPATYYCOQHNEYPLTFGGTKVEIKR 108
Db 81 RFGSGSGTDFTLTISSLQPEDPATYYCOQYNVPRTPFGGTKVEIKR 128

RESULT 10
S40336
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40336
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40336
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-124 <KLE>
A;Cross-references: UNIPARC:UPI0000116156; EMBL:X72446; NID:g441360; PIDN:CAAS1114.1; PIDD:CAAS1114.1; PIR:P00001
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 484.5; DB 2; Length 124;
Best Local Similarity 88.1%; Pred. No. 1.6e-33;
Matches 96; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYGSGTLQSGVPS 60
Db 16 DIQWTQSPSSLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIIYAASTLQSGVPS 75

Qy 61 RFGSGSGTDFTLTISSLQPEDPATYYCOQHNEY-PLTFGGTKVEIKR 108
Db 76 RFGSGSGTEFLTISSLQPEDPATYYCOQLNTYPPWTFGGTKVEIKR 124

RESULT 11
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36264
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36264
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DF4; EMBL:X18845; NID:g33426; PIDN:CAA79297.1; PIDD:CAA79297.1; PIR:P00001
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 483; DB 2; Length 107;
Best Local Similarity 86.0%; Pred. No. 1.9e-33;
Matches 92; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYGSGTLQSGVPS 60
Db 16 DIQWTQSPSSLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIIYAASTLQSGVPS 75

R-Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage particles

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19674

A:Molecule type: mRNA

A:Residues: 1-108 <VAR>

A:CROSS-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:CAAA43823.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 486; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.1e-33;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Cy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQQKPKAPKLLIYGSTLTSGVPS 60
Db 1 EIVLTQSPSSLSASVGRVTITCRASSISNYLNWYQQKPKAPKLLIYAASLTSGVPS 60
Qy 61 RFGSGSGTGDTFTLTISLQPEDPATYYCQHNEYPPLTFGGGTKVEIKR 108
Db 61 RFGSGSGTGDTFTLTINSLQPEDPATYYCQTNSPFLTFGGGTKLEIKR 108

RESULT 8

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40331

R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:CROSS-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDN:CAAS1109.1; PID:CAAS1109.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 486; DB 2; Length 123;
Best Local Similarity 88.8%; Pred. No. 1.2e-33;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Cy 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQQKPKAPKLLIYGSTLTSGVPS 60
Db 17 DIQMTQSPSSLSASVGRVTITCRASSISNYLNWYQQKPKAPKLLIYAASLTSGVPS 76
Qy 61 RFGSGSGTGDTFTLTISLQPEDPATYYCQHNEYPPLTFGGGTKVEIK 107
Db 77 RFGSGSGTGDTFTLTISLQPEDPATYYCQSYSPTPTFGGTKVEIK 123

RESULT 9

S40352

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40352

R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40352

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:CROSS-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:g441392; PIDN:CAAS1130.1; PID:CAAS1130.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

```

Db      1  EIVLTQSPSSLSASVGDRVTITCRASQISISYLNWYQOKPKGAPKLLIYAASSLQSGVPS 60
Qy      61  RFSGSGSGTDFTLTITSIISLQPEDFATYYCQQHNEYPLTFGGGQTKVEIK 107
      |||||
Db      61  RFSGSGSGTDFTLTITSIISLQPEDFATYYCQQSYNYPLTFGGGQTKVDIK 107
      |||||

RESULT 12
S40334
IG kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40334
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: UNIPARC:UPI000176CA9; EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

      Query Match      86.2%; Score 483; DB 2; Length 132;
      Best Local Similarity 85.2%; Pred. No. 2.3e-33;
      Matches 92; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy      1  DIQWTSPLSASVGDRVTITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60
      |||||
Db      22  DIQLTQSPSLASIGDRVTITCRASQINSYLAWYQKPKAPKLLIYVASTLQSGVPS 81
      |||||

Qy      61  RFSGSGSGTDFTLTITSIISLQPEDFATYYCQQHNEYPLTFGGGQTKVEIKR 108
      |||||
Db      82  RFSGSGSGTDFTLTITSIISLQPEDFASYCQQFNSYPTFFGGGQTKVEIRR 129
      |||||

RESULT 13
KLHUBN
IG kappa chain V-I region (Ban) - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A01878
R:Dwulet, F.E.; O'Connor, T.P.; Benson, M.D.
Mol. Immunol. 23, 73-78, 1986
A:Title: Polymorphism in a kappa I primary (AL) amyloid protein (BAN).
A:Reference number: A01878; MUID:96174817; PMID:3083240
A:Accession: A01878
A:Molecule type: protein
A:Residues: 1-108 <DWU>
A:Cross-references: UNIPROT:P04430; UNIPARC:UPI000012B150
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical 1
chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associat
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4
F:23-88/Disulfide bonds: #status predicted

      Query Match      85.9%; Score 481; DB 1; Length 108;
      Best Local Similarity 83.3%; Pred. No. 2.8e-33;

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DE 61 RPSGSGTDFLTITISLQPEDEATYYCQYNSYPITFGQGTKVLK 107

Search completed: April 13, 2006, 17:19:34
Job time : 23.1092 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 17:05:24 ; Search time 219.773 Seconds
(without alignments)
215.918 Million cell updates/sec

Title: US-10-727-737-2

Perfect score: 560

Sequence: 1 DIQQTSPSSLSASVGRVT.....QOHNEYPLTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21.*

1: geneseqp1980s.*

2: geneseqp1980s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|--------------------|
| 1 | 560 | 100.0 | 108 | 2 | AAW62017 Light cha |
| 2 | 560 | 100.0 | 108 | 2 | AAW63529 Humanised |
| 3 | 560 | 100.0 | 108 | 3 | AAW82343 Humanised |
| 4 | 560 | 100.0 | 108 | 8 | ADG38990 Humanised |
| 5 | 560 | 100.0 | 108 | 8 | ADG38990 Humanised |
| 6 | 560 | 100.0 | 108 | 8 | ADG38990 Humanised |
| 7 | 560 | 100.0 | 108 | 9 | ADG38990 Humanised |
| 8 | 560 | 100.0 | 108 | 9 | ADG38990 Humanised |
| 9 | 546.5 | 97.6 | 109 | 2 | AAW77752 Human lig |
| 10 | 546.5 | 97.6 | 109 | 3 | AAW77752 Human lig |
| 11 | 546.5 | 97.6 | 109 | 3 | AAW77752 Human lig |
| 12 | 546.5 | 97.6 | 109 | 6 | ABU13786 Human lig |
| 13 | 546.5 | 97.6 | 109 | 6 | ABU13786 Human lig |
| 14 | 546.5 | 97.6 | 109 | 7 | AAE39082 Human lig |
| 15 | 512 | 91.4 | 240 | 4 | AAW46020 Human MUC |
| 16 | 506 | 90.4 | 108 | 2 | AAW70622 Human con |
| 17 | 506 | 90.4 | 108 | 3 | AAW82345 Human con |
| 18 | 506 | 90.4 | 108 | 5 | ABP61191 Human ant |
| 19 | 506 | 90.4 | 108 | 8 | ADG38991 Human con |
| 20 | 506 | 90.4 | 108 | 8 | ADG38991 Human con |
| 21 | 506 | 90.4 | 108 | 8 | ADG38991 Human con |
| 22 | 506 | 90.4 | 108 | 8 | ADG38991 Human con |
| 23 | 506 | 90.4 | 109 | 9 | AAU74544 Human sub |
| 24 | 506 | 90.4 | 110 | 5 | AAE28149 Human con |

| | | | | | | |
|----|-----|------|-----|---|----------|--------------------|
| 25 | 505 | 90.2 | 127 | 4 | AAU09917 | Aau09917 Light cha |
| 26 | 505 | 90.2 | 127 | 5 | ABG75526 | Abg75526 Humanised |
| 27 | 505 | 90.2 | 233 | 7 | ADL23195 | Adl23195 Human ant |
| 28 | 504 | 90.0 | 109 | 2 | AAR40956 | Aar40956 Human ger |
| 29 | 503 | 89.8 | 240 | 4 | AAB45991 | Aab45991 Human MUC |
| 30 | 502 | 89.6 | 108 | 9 | ADW04801 | Adw04801 PAPP-A im |
| 31 | 501 | 89.5 | 107 | 4 | AAB62087 | Aab62087 Human VI |
| 32 | 501 | 89.5 | 107 | 4 | AAB60400 | Aab60400 Consensus |
| 33 | 501 | 89.5 | 107 | 4 | AAB61585 | Aab61585 Human var |
| 34 | 501 | 89.5 | 107 | 8 | ADG71454 | Adg71454 Human ant |
| 35 | 501 | 89.5 | 107 | 8 | ADJ88008 | Adj88008 Human var |
| 36 | 501 | 89.5 | 107 | 8 | ADN12054 | Adn12054 Variable |
| 37 | 501 | 89.5 | 107 | 8 | ADP43328 | Adp43328 Human mon |
| 38 | 501 | 89.5 | 108 | 6 | ABJ18679 | Abj18679 Antibody |
| 39 | 501 | 89.5 | 109 | 2 | AAW27543 | Aaw27543 Human Ab |
| 40 | 501 | 89.5 | 240 | 4 | AAB46004 | Aab46004 Human MUC |
| 41 | 499 | 89.1 | 130 | 3 | AAW56737 | Aaw56737 Amino aci |
| 42 | 499 | 89.1 | 234 | 7 | ADM47073 | Adm47073 Mouse ant |
| 43 | 499 | 89.1 | 240 | 4 | AAB45993 | Aab45993 Human MUC |
| 44 | 497 | 88.8 | 108 | 8 | ADO36411 | Ado36411 Intracell |
| 45 | 497 | 88.8 | 108 | 9 | AEA41087 | Aea41087 Germline |

ALIGNMENTS

RESULT 1
AAW62017
ID AAW62017 standard; peptide; 108 AA.
XX
AC AAW62017;
XX
DT 01-OCT-1998 (first entry)
XX
DE Light chain variable region of humanised anti-CD11a antibody.
XX
KW Complementarity determining region; light chain variable region;
KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
KW human CD11a I domain; MHM24 epitope; alpha subunit;
KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
KW in vivo imaging; diagnosis; CD11a-associated disease.
XX
OS Mus sp.
OS Homo sapiens.
XX
FN WO9823761-A1.
XX
PD 04-JUN-1998.
XX
PF 20-OCT-1997; 97WO-US019041.
XX
PR 27-NOV-1996; 96US-00757205.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1998-322737/28.
XX
PT New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
XX also to treat conditions such as immunological or inflammatory disease.
XX
XX Claim 9; Page 48; 66pp; English.
XX
CC The present sequence represents the light chain variable region of a
CC humanised anti-CD11a antibody that binds specifically to the human CD11a
CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti
CC -CD11a antibodies are used to determine presence of CD11a in usual
CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
CC associated diseases (typically immune responses and inflammation such as
CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
CC leukaemia, etc

XX SQ Sequence 108 AA;
 Query Match 100.0%; Score 560; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGRVITTCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQWTQSPSSLSASVGRVITTCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
 QY 61 RFGSGSGTDTLTITISSLOPEDFATYYCQOHNEYPVLTFGQTKVEIKR 108
 DB 61 RFGSGSGTDTLTITISSLOPEDFATYYCQOHNEYPVLTFGQTKVEIKR 108
 RESULT 2
 AAW63529
 ID AAW63529 standard; protein; 108 AA.
 XX
 AC AAW63529;
 XX
 DT 06-OCT-1998 (first entry)
 XX
 DE Humanised MHM24 light chain.
 XX
 KW Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; light chain.
 XX
 OS Synthetic.
 XX
 PN WO9823746-A1.
 XX
 PD 04-JUN-1998.
 XX
 PP 29-OCT-1997; 97MO-US020169.
 XX
 PR 27-NOV-1996; 96US-00756150.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 1998-322726/28.
 XX
 PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 PS Disclosure; Page 53; 71pp; English.
 XX
 CC This sequence represents the light chain of the humanised antibody MHM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 560; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGRVITTCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQWTQSPSSLSASVGRVITTCRASKTISKYLAWYQKPGKAPKLLIYSGSTLQSGVPS 60
 QY 61 RFGSGSGTDTLTITISSLOPEDFATYYCQOHNEYPVLTFGQTKVEIKR 108
 DB 61 RFGSGSGTDTLTITISSLOPEDFATYYCQOHNEYPVLTFGQTKVEIKR 108
 RESULT 3
 AAY82343
 ID AAY82343 standard; protein; 108 AA.
 XX
 AC AAY82343;
 XX
 DT 22-JUN-2000 (first entry)
 XX
 DE Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.
 XX
 KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 KW antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.
 XX
 OS Homo sapiens.
 OS Mus sp.
 XX
 PN US6037454-A.
 XX
 PD 14-MAR-2000.
 XX
 PP 20-NOV-1997; 97US-00974899.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2000-282241/24.
 XX
 PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarity determining regions.
 XX
 PS Claim 5; Fig 1; 39pp; English.
 XX
 CC The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the light chain variable region of the humanised anti

CC -CD11a Ab
XX Sequence 108 AA;
SQ

Query Match 100.0%; Score 560; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQGTKEIKR 108
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQGTKEIKR 108

RESULT 4
ADG38990
ID ADG38990 standard; protein; 108 AA.
XX
AC ADG38990;
XX
DT 26-FEB-2004 (first entry)
XX
DE Humanised Mouse anti-CD11a antibody light chain variable region.
XX
KW Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
KW VL; cluster of differentiation 11a; mixed lymphocyte response assay;
KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; prodrug activating enzyme; humanised.
XX
OS Synthetic.
OS Mus sp.
XX
PN US2003207336-A1.
XX
PD 06-NOV-2003.
XX
PF 28-FEB-2001; 2001US-00795798.
XX
PR 27-NOV-1996; 96US-0031971P.
PR 20-NOV-1997; 97US-00974899.
PR 20-OCT-1999; 99US-00420745.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 2004-051511/05.
XX
PF Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
XX
PS Claim 9; SEQ ID NO 2; 43pp; English.
XX

The invention relates to a Humanised anti-cluster of differentiation (CD)11a antibody having specificity to human CD11a I-domain or CD11a with a kd value of not more than 1x10⁻⁸ M, or concentration for 50 % inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM) -1. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The antibody is useful for determining the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such

CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the light chain variable region (VL) of the humanised mouse anti-CD11a I domain monoclonal antibody MHM24.
XX Sequence 108 AA;
SQ

Query Match 100.0%; Score 560; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVTITCRASKTISKYLAWYQOKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQGTKEIKR 108
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQGTKEIKR 108

RESULT 5
ADR03365
ID ADR03365 standard; protein; 108 AA.
XX
AC ADR03365;
XX
DT 21-OCT-2004 (first entry)
XX
DE Humanised MHM24 F(ab)-8 antibody variable light chain protein.
XX
KW CD11a antibody; human immunodeficiency virus infection; HIV infection; rhinovirus infection; inflammatory skin disease; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SLE; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis;
KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak;
KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy;
KW murine anti-human CD11a monoclonal antibody; MHM24; variable light chain; VL; murine; human; fusion protein.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US2004146507-A1.
XX
PD 29-JUL-2004.
XX
PF 03-DEC-2003; 2003US-00727737.
XX
PR 27-NOV-1996; 96US-0031945P.
PR 20-NOV-1997; 97US-00975329.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 2004-552640/53.
XX

New antibody mutant of a species-dependent antibody, useful for treating PT and preventing infectious diseases, psoriasis, inflammatory bowel PT disease, allergic conditions, autoimmune diseases, or cancer. XX
PS Example; SEQ ID NO 2; 54pp; English.
XX
CC The present invention relates to an antibody mutant of a species-dependent antibody with beneficial properties. The invention is useful CC

CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanized murine anti-human CD11a monoclonal antibody
 CC (MHM24) F(ab)-8 variable light chain protein. This sequence is used in
 CC the exemplification of the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 560; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQQKPKAPKLLIYSGSTLQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQQKPKAPKLLIYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDFTLTITSSIQPEDPATYCCQHNEYPPLTFGGQTKVEIKR 108
 Db 61 RFGSGSGTDFTLTITSSIQPEDPATYCCQHNEYPPLTFGGQTKVEIKR 108

RESULT 6

ADW38457

ID ADW38457 standard; protein; 108 AA.

XX AC ADW38457;

XX DT 24-MAR-2005 (first entry)

XX DE CD11a light chain variable region #2.

XX KW monoclonal antibody; CD11a; light-chain variable region;
 XX heavy-chain variable region.

XX OS Homo sapiens.

XX PN CN1439651-A.

XX PD 03-SEP-2003.

XX PF 20-FEB-2002; 2002CN-00110866.

XX PR 20-FEB-2002; 2002CN-00110866.

XX PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.

XX PI Wang H, Wang J;

XX DR WPI; 2004-169719/17.

XX KW Recombinant human CD11a monoclonal antibody and its preparation and
 PT medicinal composition.

XX PS Claim 1; Page 14; 16pp; Chinese.

XX CC The present invention relates to a recombinant monoclonal antibody for
 CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
 CC No.5 in light-chain variable region and the amino acid sequence shown by
 CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
 CC bioactivity and the expression in host cell are greatly increased. The
 CC DNA molecule for coding the antibody, its preparation process and the
 CC medicinal composition containing it are also disclosed. The present
 CC sequence represents a light chain variable region of human CD11a.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 560; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQQKPKAPKLLIYSGSTLQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQQKPKAPKLLIYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDFTLTITSSIQPEDPATYCCQHNEYPPLTFGGQTKVEIKR 108
 Db 61 RFGSGSGTDFTLTITSSIQPEDPATYCCQHNEYPPLTFGGQTKVEIKR 108

RESULT 7

ADX80645

ID ADX80645 standard; protein; 108 AA.

XX AC ADX80645;

XX DT 05-MAY-2005 (first entry)

XX DE Humanized CD11a variable light chain amino acid sequence, seq id 5.

XX KW Protein purification; leaching; protein A affinity chromatography; CD11a;
 XX antibody.

XX OS Synthetic.

XX PN US2005038231-A1.

XX PD 17-FEB-2005.

XX PF 24-JUN-2004; 2004US-00877532.

XX PR 28-JUL-2003; 2003US-0490500P.

XX PA (GETH) GENENTECH INC.

XX PI Fahrner RL, Laverdiere A, McDonald PU, O'leary RM;

XX DR WPI; 2005-172327/18.

XX PT Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
 PT the temperature of a composition subjected to protein A affinity
 PT chromatography to 3-20 degrees C, where protein A leaching is reduced.

XX PS Disclosure; SEQ ID NO 5; 27pp; English.

XX CC The invention relates to a method of purifying a protein which comprises
 CC a CH2/CH3 region by protein A affinity chromatography. The method
 CC involves reducing the temperature of a composition comprising the protein
 CC and one or more impurities subjected to protein A affinity chromatography
 CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
 CC the protein is antibody. The antibody is selected from Trastuzumab,
 CC humanized 2C4, humanized CD11a antibody, and humanized VEGF antibody.
 CC Preferably, the antibody binds HER2 antigen, where the antibody is
 CC Trastuzumab or humanized 2C4. The protein is an immunoadhesin,
 CC specifically a TNF receptor immunoadhesin. The methods are useful for
 CC purifying a protein, which comprises a CH2/CH3 region by protein A
 CC affinity chromatography and for reducing leaching of protein A during
 CC protein A affinity chromatography. The current sequence represents the
 CC variable light chain amino acid sequence of CD11a.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 560; DB 9; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQQKPKAPKLLIYSGSTLQSGVPS 60


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XX AC AAY7752;
XX AD 06-JUN-2000 (first entry)
XX DE Human light chain k1 consensus framework.
XX KW Interleukin-8; IL-8; monoclonal antibody; Mab; anti-IL-8; 6G4.2.5V11N35A;
XX KW inflammatory disorder; adult respiratory distress syndrome; chimeric;
XX KW affinity purification; 6G4.2.5.
XX OS Homo sapiens.
XX PN US6025158-A.
XX PD 15-FEB-2000.
XX PF 20-FEB-1998; 98US-00027449.
XX PR 21-FEB-1997; 97US-0038664P.
XX PR 22-JAN-1998; 98US-0074330P.
XX PA (GETH ) GENENTECH INC.
XX PI Presta LG, Leong SR, Gonzalez TN;
XX DR WPI; 2000-181809/16.
XX CC New nucleic acid molecule encodes a polypeptide which is an anti-
PT interleukin-8 monoclonal antibody or antibody fragment useful for the
PT production of anti-interleukin-8 monoclonal antibodies or fragments.
XX PS Example; Fig 29; 188pp; English.
XX CC The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs
CC (complementarity determining regions) of the humanized anti-IL-8
CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized anti-
CC IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 Mabs and fragments can be
CC used in diagnosis, for affinity purification of IL-8 from recombinant
CC cell culture or natural sources and for the treatment of inflammatory
CC disorders e.g. adult respiratory distress syndrome. Nucleic acids
CC encoding the anti-IL-8 Mab can be associated in a vector with another
CC gene encoding another protein or protein fragment to produce a fusion
CC protein which can make isolation and/or purification of the protein an
CC easier process
XX SQ Sequence 109 AA;
Query Match 97.6%; Score 546.5; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.6e-32;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKFGKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKFGKAPKLLIYSGSTLQSGVP 60
Qy 60 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPLTFGGTKVEIKR 108
Db 61 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPLTFGGTKVEIKR 109
RESULT 11
AAB30309
ID AAB30309 standard; protein; 109 AA.
XX AC AAB30309;
XX AD 12-FEB-2001 (first entry)
XX DE Human light chain kappa1 consensus framework SEQ ID NO: 47.
XX KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;

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KW adult respiratory distress syndrome; multiple organ failure;
KW bacterial pneumonia; inflammatory bowel disease.
XX OS Homo sapiens.
XX PN US6133426-A.
XX PD 17-OCT-2000.
XX PF 20-FEB-1998; 98US-00026985.
XX PR 21-FEB-1997; 97US-0038664P.
XX PR 22-JAN-1998; 98US-0074330P.
XX PA (GETH ) GENENTECH INC.
XX PI Presta LG, Leong SR, Gonzalez TN;
XX DR WPI; 2000-686027/67.
XX CC Humanized anti-interleukin 8 monoclonal antibody variant useful for
PT treating inflammatory disorders, such as adult respiratory distress
PT syndrome, hypovolemic shock and ulcerative colitis.
XX PS Disclosure; Col 161-162; 240pp; English.
XX CC The present invention provides a number of humanised monoclonal anti-IL-8
CC antibodies which can be used in the diagnosis and treatment of
CC inflammatory disorders, including adult respiratory distress syndrome,
CC septic shock, multiple organ failure, bacterial pneumonia and
CC inflammatory bowel disease. The present sequence comprises one of the
CC antibodies of the invention
XX SQ Sequence 109 AA;
Query Match 97.6%; Score 546.5; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.6e-32;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKFGKAPKLLI-YSGSTLQSGVP 59
Db 1 DIQWTQSPSSLSASVGRVITTCRASTISKYLAWYQKFGKAPKLLIYSGSTLQSGVP 60
Qy 60 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPLTFGGTKVEIKR 108
Db 61 SRFSGSGGTDFTLTITSSLPEDPATYCCQHNEYPLTFGGTKVEIKR 109
RESULT 12
ABU13786
ID ABU13786 standard; protein; 109 AA.
XX AC ABU13786;
XX AD 25-FEB-2003 (first entry)
XX DE Human light chain kappa1 consensus framework sequence.
XX KW Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mAb;
XX antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
XX PSG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
XX inflammatory disease; inflammatory bowel disease; psoriasis; scleriosis;
XX ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
XX osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
XX alcoholic hepatitis; cystic fibrosis; human.
XX OS Homo sapiens.
XX PN US6468532-B1.
XX PD 22-OCT-2002.
XX PR 20-JAN-1999; 99US-00234340.

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XX 22-JAN-1998; 98US-0074330P.
 PR 20-FEB-1998; 98US-0075467P.
 PR 24-JUL-1998; 98US-0094003P.
 PR 24-JUL-1998; 98US-0094013P.
 PA (GETH) GENENTECH INC.
 XX Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 PI WPI; 2003-138230/13.
 DE Treating acute lung injury in mammal by administering to mammal a 500 kD
 PT conjugate comprising F(ab')₂ antibody fragment that binds to human
 PT interleukin-8, covalently attached to one or two polyethylene glycol
 PT molecules.
 XX
 XX Example G; Fig 29; 259pp; English.
 XX
 CC The invention relates to treating acute lung injury in a mammal,
 CC comprising administering to the mammal an effective amount of a conjugate
 CC of a single antibody fragment covalently attached to 1 or 2 polyethylene
 CC glycol (PEG) molecules, where the antibody fragment is a F(ab')₂
 CC comprising: (a) first chain that is either a light chain or a heavy chain
 CC ; (b) a first opposite chain that is either a heavy chain opposite the
 CC first light chain or a light chain opposite the first heavy chain; (c) a
 CC second chain that is either a light chain or a heavy chain; and (d) a
 CC second opposite chain that is either a heavy chain opposite the second
 CC light chain or a light chain opposite the second heavy chain; where every
 CC PEG molecule is covalently attached to a first cysteine residue in the
 CC first or second chain that would ordinarily form a disulphide bridge with
 CC a second cysteine residue in the first or second opposite chain, where
 CC the disulphide bridge is avoided by substitution of another amino acid
 CC residue for the second cysteine residue in the first or second opposite
 CC chain, where the F(ab')₂ comprises an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and where the apparent size of the conjugate
 CC is at least about 500 kD. The antigen binding sites may be derived from
 CC murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
 CC treating lung injury, including adult respiratory distress syndrome
 CC (ARDS) in a mammal and inflammatory diseases (such as asthma,
 CC inflammatory bowel disease, psoriasis and sclerosis), ischaemic
 CC reperfusion disorders, stroke, multiple sclerosis, meningitis,
 CC osteoarthritis, septic shock, autoimmune disease (e.g. rheumatoid
 CC arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
 CC and disorders listed in the specification. The present sequence
 CC represents a human antibody sequence included for comparison with the
 CC mouse humanised monoclonal antibody sequences
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 97.6%; Score 546.5; DB 6; Length 109;
 Best Local Similarity 98.2%; Pred. No. 4.6e-32;
 Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 DIQWTSPLSASVGRVITCRASKTISKYLAWYQKFGKAPKLLI-YSGSTLQSGVP 59
 DB 1 DIQWTSPLSASVGRVITCRASKTISKYLAWYQKFGKAPKLLIYSGSTLQSGVP 60
 QY 60 SRPFGSGGDFTLTISLQPEDPATYVCOQHNEYPITFGGKTVEIKR 108
 DB 61 SRPFGSGGDFTLTISLQPEDPATYVCOQHNEYPITFGGKTVEIKR 109
 RESULT 13
 ABU59499
 ID ABU59499 standard; protein; 109 AA.
 AC
 AC ABU59499;
 XX
 XX 22-APR-2003 (first entry)
 DT
 XX Human light chain kappaI consensus framework.
 DE
 XX

KW Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
 KW inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
 KW systemic scleroderma; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
 KW stroke; adult respiratory distress syndrome; rheumatoid arthritis;
 KW alcoholic hepatitis; acute lung injury; asthma; cerebral oedema;
 KW myocardial ischaemia; cranial trauma; asphyxia; Behcet's disease;
 KW dermatomyositis; polymyositis; multiple sclerosis; meningitis;
 KW encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma;
 KW autoimmune disease; Sjogren's syndrome; vasculitis; septicemia;
 KW central nervous system inflammatory disorder; sepsis; sarcoidosis;
 KW multiple organ injury syndrome; bacterial pneumonia; glomerulonephritis;
 KW inflammation of the lung; human.
 XX Homo sapiens.
 OS
 XX US6458355-B1.
 PN
 XX 01-OCT-2002.
 PD
 XX 24-JUL-1998; 98US-00121952.
 XX
 XX 22-JAN-1998; 98US-0074330P.
 PR
 PR 20-FEB-1998; 98US-0075467P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 PI WPI; 2003-208759/20.
 DR
 XX Treating inflammatory disorder in a mammal, involves administering a
 PT conjugate of polyethylene glycol and a single antibody fragment
 PT comprising antigen binding site that binds to human interleukin-8, to
 PT mammal.
 XX
 XX Example 3G; Fig 29; 259pp; English.
 XX
 CC The invention relates to treating an inflammatory disorder in a mammal,
 CC comprising administering to the mammal, an effective amount of a
 CC conjugate of a single antibody fragment (e.g. the heavy or light chains
 CC of the humanised mouse monoclonal antibodies 5.12.14 and 6G4.2.5, which
 CC also have their intramolecular disulphide bridges ablated by substitution
 CC mutations) covalently attached to one or two polyethylene glycol (PEG)
 CC molecules. The antibodies comprise an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and the apparent size of the conjugate is at
 CC least 500 kDa. The method is useful for treating an inflammatory disorder
 CC e.g. ischaemic reperfusion disorder such as surgical tissue reperfusion
 CC injury, myocardial ischaemia or myocardial infarction, or hypovolemic
 CC shock, in a mammal e.g. human. The method is useful for treating
 CC inflammatory disorders including psoriasis, atopic dermatitis, systemic
 CC scleroderma and sclerosis, responses associated with inflammatory bowel
 CC disease, ischaemic reperfusion disorders, myocardial ischaemic
 CC conditions, cerebral oedema secondary to stroke, cranial trauma,
 CC asphyxia, adult respiratory distress syndrome, acute lung injury,
 CC Behcet's disease, dermatomyositis, polymyositis, multiple sclerosis,
 CC dermatitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
 CC nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
 CC syndrome, vasculitis, central nervous system inflammatory disorder,
 CC multiple organ injury syndrome secondary to septicemia or trauma,
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
 CC mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
 CC immunopathologic responses to tissue/organ transplantation, inflammations
 CC of the lung, inflammatory bowel disease such as ulcerative colitis and
 CC asthma. The present sequence represents the light or heavy chain of human
 CC IGG, used to design the humanising mutations in the two mouse antibodies
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 97.6%; Score 546.5; DB 6; Length 109;
 Best Local Similarity 98.2%; Pred. No. 4.6e-32;
 Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQWTSFSSLSASVGRVTTTCRAKTIISKYLAWYQKPGKAPKLLI-YSGSTLQSGVP 59
 Db 1 DIQWTSFSSLSASVGRVTTTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVP 60
 Qy 60 SRFSGSGSGTDFTLTISSLOPEDPATYCCQHNEYPITFGQGTKEIKR 108
 Db 61 SRFSGSGSGTDFTLTISSLOPEDPATYCCQHNEYPITFGQGTKEIKR 109

RESULT 14
 AA39082
 ID AAE39082 standard; protein; 109 AA.
 AC AAE39082;
 XX
 DT 18-DEC-2003 (first entry)
 DE Human light chain kappaI consensus framework protein.

XX Interleukin-8 mediated disease; adult respiratory distress syndrome; IL;
 KW bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
 KW ulcerative colitis; ischaemic reperfusion injury; myocardial infarction;
 KW acute lung injury; inflammatory disease; asthma; antibody; human.
 XX
 OS Homo sapiens.

XX US2003021790-A1.
 XX 30-JAN-2003.
 XX 29-NOV-2000; 2000US-00726258.
 XX 22-JAN-1998; 98US-0074330P.
 PR 20-FEB-1998; 98US-0075457P.
 PR 24-JUL-1998; 98US-0094003P.
 PR 24-JUL-1998; 98US-0094013P.
 PR 20-JAN-1999; 99US-00234182.
 XX (GERTH) GENENTECH INC.

XX Haei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 PI WPI; 2003-605694/57.

XX Novel conjugates comprising antibody fragments covalently attached to
 PT nonproteinaceous polymer molecules, useful for treating inflammatory
 PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
 PT asthma.

XX Example; Fig 29; 266pp; English.
 PS
 CC The invention relates to novel conjugates comprising antibody fragments
 CC covalently attached to nonproteinaceous polymer molecules. The invention
 CC is useful for treating interleukin (IL)-8 mediated diseases or disorders
 CC such as inflammatory diseases, acute lung injury e.g. adult respiratory
 CC distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial
 CC infarction, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
 CC colitis, bacterial pneumonia and asthma. The invention is also useful as
 CC a reagent in an animal model system for in vivo study of the biological
 CC functions of the antigen recognised by the conjugate. The present
 CC sequence is human light chain kappaI consensus framework protein. This
 CC sequence is used in the exemplification of the invention

XX Sequence 109 AA;
 Query Match 97.6%; Score 546.5; DB 7; Length 109;
 Best Local Similarity 98.2%; Pred. No. 4.6e-32;
 Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIQWTSFSSLSASVGRVTTTCRAKTIISKYLAWYQKPGKAPKLLI-YSGSTLQSGVP 59
 Db 1 DIQWTSFSSLSASVGRVTTTCRAKTIISKYLAWYQKPGKAPKLLIYSGSTLQSGVP 60

Qy 60 SRFSGSGSGTDFTLTISSLOPEDPATYCCQHNEYPITFGQGTKEIKR 108
 Db 61 SRFSGSGSGTDFTLTISSLOPEDPATYCCQHNEYPITFGQGTKEIKR 109

RESULT 15
 AAB46020
 ID AAB46020 standard; peptide; 240 AA.
 AC AAB46020;
 XX
 DT 23-MAR-2001 (first entry)
 DE Human MUC-1 scFv clone N1.

XX MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
 KW antiidiotypic antibody; cytostatic; virucidal; antibacterial; TP antigen;
 KW antiparasitic; infectious disease.

XX Homo sapiens.
 XX WO2000073430-A2.
 XX 07-DEC-2000.
 XX 29-MAY-2000; 2000WO-DE001809.
 XX 27-MAY-1999; 99DE-01024405.
 PR 09-SEP-1999; 99DE-01043016.

XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX Goletz S, Karsten U;
 PI WPI; 2001-049937/06.

XX Vaccines against conformation-dependent or non-peptide antigens, based on
 PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
 PT vaccines.

XX Disclosure; Page 5-9; 36pp; German.
 PS
 CC This invention describes a novel vaccine (V1) against conformation-
 CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or
 CC peptide which immunologically imitates CDA, is new. (I) encodes a region
 CC of an antiidiotypic antibody (Ab2) or another peptide which: (a)
 CC specifically binds to the binding site of an antibody (Ab1) or an antigen
 CC binding molecule; and (b) immunologically mimics the initial antigen. The
 CC epitope is partially or completely conformation-dependent, and has an
 CC immunogenic structure defined by a specific spatial conformation of amino
 CC acids. (I) is used in the form of linear or circular naked DNA and/or
 CC with a viral vector and/or adjuvants. The products of the invention have
 CC cytostatic, virucidal, antibacterial and antiparasitic. The invention
 CC also describes (1) a corresponding vaccine (V2) against antigens which
 CC are not proteins or peptides, as defined above but which have epitopes
 CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
 CC human antiidiotypic antibody fragments against the MUC1-conformation
 CC epitope having one of 31 approximately 60 residue amino acids sequences,
 CC all fully defined in the specification; (4) MUC1-conformation epitope
 CC mimics having one of 16 9-17 residue amino acid sequences, all fully in
 CC the specification; (5) antiidiotypic antibody fragments against the TP
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TP carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible

XX Sequence 240 AA;
 SQ Query Match 91.4%; Score 512; DB 4; Length 240;

| | Best Local Similarity | 91.7%; Pred. No. 2.8e-29; | Mismatches | 99; Conservative | 2; Mismatches | 7; Indels | 0; Gaps | 0; |
|----|-----------------------|--|------------|------------------|---------------|-----------|---------|----|
| QY | 1 | DIQMTSPSSLSASVGDRTVTTCRASTKTSIKYLAWYQQKGPKAPKLIIYSGSTLQS | 60 | | | | | |
| DB | 133 | DIQMTSPSSLASVGDRTVTTCRASQSISSYLANWYQKGPKAPKLIIYGASVLQSG | 192 | | | | | |
| QY | 61 | RFSGSGSSTDFTLTILSIQLQDPDPAFYTCQHNHNYPLTFGGQTKVEIKR | 108 | | | | | |
| DE | 193 | RFSGSGSSTDFTLTILSIQLQDPDPAFYTCQHNHNYPLTFGGQTKVEIKR | 240 | | | | | |

| Search completed: April 13, 2006, 17:13:39
| Job time : 222.273 secs

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